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(54) Title: PATHOGEN TOLERANCE GENES

(57) Abstract: The present invention relates to transgenic plants and methods of making transgenic plant using punitive transcription factors that modulate the transgenic plant's susceptibility to disease.

<b>PATHOGEN TOLERANCE GENES</b>
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**RELATED APPLICATION INFORMATION**

The present invention claims the benefit from US Provisional Patent Application  
5 Serial Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and  
"Plant Trait Modification III" filed August 22, 2000.

**FIELD OF THE INVENTION**

This invention relates to the field of plant biology. More particularly, the  
present invention pertains to compositions and methods for phenotypically modifying a plant.

**BACKGROUND OF THE INVENTION**

10 Transcription factors can modulate gene expression, either increasing or  
decreasing (inducing or repressing) the rate of transcription. This modulation results in  
differential levels of gene expression at various developmental stages, in different tissues and  
cell types, and in response to different exogenous (e.g., environmental) and endogenous  
15 stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological  
pathways, altering the expression levels of one or more transcription factors can change entire  
biological pathways in an organism. For example, manipulation of the levels of selected  
transcription factors may result in increased expression of economically useful proteins or  
20 metabolic chemicals in plants or to improve other agriculturally relevant characteristics.  
Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis  
of unwanted compounds or remove an undesirable trait. Therefore, manipulating  
transcription factor levels in a plant offers tremendous potential in agricultural biotechnology  
for modifying a plant's traits.

25 The present invention provides novel transcription factors useful for  
modifying a plant's phenotype in desirable ways, such as modifying a plant's pathogen  
tolerance.

**SUMMARY OF THE INVENTION**

In a first aspect, the invention relates to a recombinant polynucleotide  
30 comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide  
sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N,  
where N=1-29, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence  
encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of  
(a); (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-  
35 1, where N=1-29, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence

comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a  
5 nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's pathogen tolerance; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which  
10 encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where  
15 N=1-29. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the  
20 recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention may  
25 be a plant lacking a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29.

The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce,  
30 mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

35 In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having improved pathogen tolerance. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified pathogen tolerance.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant pathogen tolerance phenotype.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant pathogen tolerance phenotype.

### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

### DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's pathogen tolerance when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying traits associated with a plant's pathogen tolerance, such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, alterations in the cell death response, or the like. Transgenic plants employing the polynucleotides or polypeptides of the invention are more tolerant to biotrophic or necrotrophic pathogens such as fungi, bacteria, mollicutes, viruses, nematodes, parasitic higher plants or the like.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol.

Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. 9: 597-604);  
 5 the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al.  
 10 (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

15 In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially  
 20 complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, of as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

#### DEFINITIONS

25 A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide  
 30 may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA,  
 35 a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant

tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2%

increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification  
5 observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought,  
10 water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest.

Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenolipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble)  
15 and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be  
20 modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

### 30 POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's pathogen tolerance.

35 Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence

analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

5 Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed  
10 to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention were ectopically expressed in  
15 overexpressor or knockout plants and changes in the pathogen tolerance of the plants was observed. Therefore, the polynucleotides and polypeptides can be employed to improve the pathogen resistance of plants.

#### Making polynucleotides

The polynucleotides of the invention include sequences that encode  
20 transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both  
25 sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such  
30 as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the  
35 art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger");

Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

#### HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn,

potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 31% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

#### Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription

factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

### SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

**Table 1**

Amino acids			Codon							
Alanine	Ala	A	GCA	GCC	GCG	GCU				
Cysteine	Cys	C	TGC	TGT						
Aspartic acid	Asp	D	GAC	GAT						
Glutamic acid	Glu	E	GAA	GAG						
Phenylalanine	Phe	F	TTC	TTT						
Glycine	Gly	G	GGA	GGC	GGG	GGT				
Histidine	His	H	CAC	CAT						
Isoleucine	Ile	I	ATA	ATC	ATT					
Lysine	Lys	K	AAA	AAG						
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT		
Methionine	Met	M	ATG							
Asparagine	Asn	N	AAC	AAT						
Proline	Pro	P	CCA	CCC	CCG	CCT				
Glutamine	Gln	Q	CAA	CAG						
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT		
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT		
Threonine	Thr	T	ACA	ACC	ACG	ACT				
Valine	Val	V	GTA	GTC	GTG	GTT				
Tryptophan	Trp	W	TGG							
Tyrosine	Tyr	Y	TAC	TAT						

15

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

20

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

**Table 2**

<b>Residue</b>	<b>Conservative Substitutions</b>
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) *Nature* 370:389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of

the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51: 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

#### EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

##### Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant

Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

5                   Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a  
10                   good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

15                   Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a  
20                   transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

                  Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (see, e.g., Odel et al. (1985) Nature  
25                   313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

                  A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on  
30                   the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For  
35                   example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the

2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlmeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

#### Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation

codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

#### Expression Hosts

5 The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral  
10 particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook  
15 and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation  
20 (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO  
25 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

30 The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

35 For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the

expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

#### Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids.

The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

#### IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After

identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

#### IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the

expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northern, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

#### SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A

subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

## PRODUCTION OF TRANSGENIC PLANTS

### Modification of Traits

5           The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the pathogen resistance of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared  
10       with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved pathogen tolerance, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

### Antisense and Cosuppression Approaches

15           In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof,  
20       can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple  
25       oligonucleotide sequences and catalytic sequences such as ribozymes.

          For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or  
30       homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of  
35       shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various

lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense  
5 construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific  
10 endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription  
15 factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the  
20 introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA,  
25 e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing  
30 a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion  
35 mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single

transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Patent No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco,

peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture --Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

5 Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are  
10 not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the  
15 sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526;  
20 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the  
25 antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by  
30 analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

#### INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of  
35 one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may

be used to associate or link certain functional benefits, such improved pathogen tolerance, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin  
5 Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local  
10 homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed  
15 by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

20 A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of  
25 skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information  
30 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for  
35 initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters

M (reward score for a pair of matching residues; always  $> 0$ ) and N (penalty score for mismatching residues; always  $< 0$ ). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may be implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or

wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

#### EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

##### EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with <sup>32</sup>P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO<sub>4</sub> pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

#### EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

#### EXAMPLE III. TRANSFORMATION OF AGROBACTERIUM WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml

LB medium (Sigma) overnight at 28°C with shaking until an absorbance ( $A_{600}$ ) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled  
5 buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

*Agrobacterium* cells were transformed with plasmids prepared as described  
10 above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After  
15 electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR  
20 amplification and sequence analysis.

#### EXAMPLE IV. TRANSFORMATION OF ARABIDOPSIS PLANTS WITH AGROBACTERIUM TUMEFACIENS WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to  
25 transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance ( $A_{600}$ ) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM  
30 benzylamino purine (Sigma), 200 µl/L Silwet L-77 (Lehle Seeds) until an absorbance ( $A_{600}$ ) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under  
35 continuous illumination (50-75 µE/m<sup>2</sup>/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of

multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

#### EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H<sub>2</sub>O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H<sub>2</sub>O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75  $\mu\text{E}/\text{m}^2/\text{sec}$ ) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T<sub>1</sub> generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T<sub>2</sub>) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

#### EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 bases to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

#### 15 EXAMPLE VII. IDENTIFICATION OF PATHOGEN INDUCED GENES

In some instances, expression patterns of the pathogen induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imogene a software purchased from BioDiscovery (Los Angeles, CA).

EXAMPLE VIII. IDENTIFICATION OF PATHOGEN TOLERANCE PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotrophic fungal pathogens, such as *Erysiphe orontii*; and necrotrophic fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

*Erysiphe orontii* is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

*Botrytis cinerea* is a necrotrophic pathogen. *Botrytis cinerea* was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (-sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens *Pseudomonas syringae* pv *maculicola* strain 4326 and pv *maculicola* strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

**Table 3**

SEQ ID No.	GID	Knockout (KO) or overexpressor (OE)	Phenotype
1	G188	KO	Increased susceptibility to Fusarium
3	G616	OE	Increased tolerance to Erysiphe
5	G19	OE	Increased tolerance to Erysiphe
7	G261	OE	Increased susceptibility to Botrytis
9	G28	OE	Increased resistance to Erysiphe
11	G869	OE	Increased susceptibility to Fusarium
13	G237	OE	Increased tolerance to Erysiphe
15	G409	OE	Increased tolerance to Erysiphe
17	G418	OE	Increased tolerance to Pseudomonas
19	G591	OE	Increased tolerance to Erysiphe
21	G525	OE	Increased tolerance to Pseudomonas
23	G545	OE	Increased susceptibility to Pseudomonas, Erysiphe and Fusarium
25	G865	OE	Increased susceptibility to Erysiphe and Botrytis
27	G881	OE	Increased susceptibility to Erysiphe and Botrytis
29	G896	KO	Increased susceptibility to Fusarium
31	G378	OE	Increased resistance to Erysiphe
33	G569	OE	Decreased expression of defense genes
35	G558	OE	Increased expression of defense genes

5 For a particular overexpressor that shows an increased susceptibility to a pathogen, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows an increased susceptibility to a pathogen, it may be more useful to select a plant with an increased expression of the particular transcription factor.

10 Other than *Fusarium oxysporum*, *Erysiphe orontii*, the transgenic plants are more tolerant to *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp.*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp.*, *Fusarium solani*, or the like. The transgenic plants are more resistant to fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf

15 blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial wilt, soft rot of vegetables, and the like; nematode diseases such as root knot, sugar beet cyst nematode or the like.

20

**EXAMPLE IX. IDENTIFICATION OF HOMOLOGOUS SEQUENCES**

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-58 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs Nos. 1-58, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is  $3.6 \times 10^{-40}$ . For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-*Arabidopsis* genes shown in Figure 3 and the *Arabidopsis* genes in the sequence listing are: SEQ ID No. 1: 38%-76%; SEQ ID No. 3: 36%-72%; SEQ ID No. 5: 51%-75%; SEQ ID No. 7: 37%-76%; SEQ ID No. 9: 48%-75%; SEQ ID No. 11: 31%-68%; SEQ ID No. 13: 59%-81%; SEQ ID No. 15: 49%-81%; SEQ ID No. 17: 53%-87%; SEQ ID No. 19: 48%-84%; SEQ ID No. 21: 73%-89%; SEQ ID No. 23: 52%-64%; SEQ ID No. 25: 48%-83%; SEQ ID No. 27: 35%-92%; SEQ ID No. 29: 56%-89%; SEQ ID No. 31: 50%-90%; SEQ ID No. 33: 50%-93%; SEQ ID No. 35: 52%-81%; SEQ ID No. 37: 75%-81%; SEQ ID No. 39: 35%-72%; SEQ ID No. 41: 55%-89%; SEQ ID No. 43: 56%-77%; SEQ ID No. 45: 34%-72%; SEQ ID No. 47: 51%-86%; SEQ ID No. 49: 46%-86%; SEQ ID No. 51: 58%-80%; SEQ ID No. 53: 46%-55%; SEQ ID No. 55: 84%-89%; and SEQ ID No. 57: 43%-71%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the pathogen tolerance of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A transgenic plant with modified pathogen tolerance, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - 5 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29, or a complementary nucleotide sequence thereof;
  - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
  - 10 (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-29, or a complementary nucleotide sequence thereof;
  - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
  - (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide  
15 sequence of one or more of: (a), (b), (c), or (d);
  - (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
  - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's  
20 pathogen tolerance;
  - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
  - (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
  - 25 (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29;
  - (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and
  - 30 (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-29.
2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.
- 35 3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot,

cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

- 5      4.      An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
- 10            (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-29, or a complementary nucleotide sequence thereof;
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-29, or a complementary nucleotide sequence thereof;
- 15            (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
- 20            (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's pathogen tolerance;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- 25            (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-29; and
- 30            (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-29.
- 35      5.      The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.

6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.
7. A cell comprising the cloning or expression vector of claim 6.
8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.
9. A composition produced by one or more of:
- (a) incubating one or more polynucleotide of claim 4 with a nuclease;
  - (b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;
  - (c) incubating one or more polynucleotide of claim 4 with a polymerase;
  - (d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;
  - (e) incubating one or more polynucleotide of claim 4 with a cloning vector, or
  - (f) incubating one or more polynucleotide of claim 4 with a cell.
10. A composition comprising two or more different polynucleotides of claim 4.
11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.
12. A plant comprising an isolated polypeptide of claim 11.
13. A method for producing a plant having a modified pathogen tolerance, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for improved pathogen tolerance thereby providing the modified plant with a modified pathogen tolerance.
14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.
15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:
- (a) expressing a polypeptide encoded by the polynucleotide in a plant; and
  - (b) identifying at least one factor that is modulated by or interacts with the polypeptide.

16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.
- 5 17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.
18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:
- 10 (a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,
- (b) monitoring one or more of:
- (i) expression level of the polynucleotide in the plant;
- (ii) expression level of the polypeptide in the plant;
- 15 (iii) modulation of an activity of the polypeptide in the plant; or
- (iv) modulation of an activity of the polynucleotide in the plant.
19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide
- 20 encoded by the polynucleotide.
20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant pathogen tolerance phenotype.
- 25 21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:
- (a) providing a sequence database; and,
- 30 (b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.
- 35 22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.

5

24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant pathogen tolerance phenotype.

10 25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.

26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.

15

27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G188	cDNA	
2	G188	protein	175-222
3	G616	cDNA	
4	G616	protein	39-95
5	G19	cDNA	
6	G19	protein	76-145
7	G261	cDNA	
8	G261	protein	16-104
9	G28	cDNA	
10	G28	protein	145-213
11	G869	cDNA	
12	G869	protein	109-177
13	G237	cDNA	
14	G237	protein	11-113
15	G409	cDNA	
16	G409	protein	64-124
17	G418	cDNA	
18	G418	protein	500-560
19	G591	cDNA	
20	G591	protein	143-240
21	G525	cDNA	
22	G525	protein	23-167
23	G545	cDNA	
24	G545	protein	82-102, 136-154
25	G865	cDNA	
26	G865	protein	36-103
27	G881	cDNA	
28	G881	protein	176-233
29	G896	cDNA	
30	G896	protein	18-39
31	G378	cDNA	
32	G378	protein	196-237
33	G569	cDNA	
34	G569	protein	90-153
35	G558	cDNA	
36	G558	protein	45-105

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
37	G1396	homolog of G1394	cDNA	
38	G1396	homolog of G1394	protein	entire protein
39	G265	homolog of G261	cDNA	
40	G265	homolog of G261	protein	14-105
41	G1006	homolog of G28	cDNA	
42	G1006	homolog of G28	protein	114-182
43	G1309	homolog of G237	cDNA	
44	G1309	homolog of G237	protein	9-114
45	G2550	homolog of G418	cDNA	
46	G2550	homolog of G418	protein	348-408
47	G965	homolog of G418	cDNA	
48	G965	homolog of G418	protein	423-486
49	G793	homolog of G591	cDNA	
50	G793	homolog of G591	protein	151-206
51	G764	homolog of G525	cDNA	
52	G764	homolog of G525	protein	27-171
53	G350	homolog of G545	cDNA	
54	G350	homolog of G545	protein	91-113,150-170
55	G986	homolog of G881	cDNA	
56	G986	homolog of G881	protein	146-203
57	G1349	homolog of G896	cDNA	
58	G1349	homolog of G896	protein	13-63

Figure 3A

SEQ ID No.	GID	Genbank NID	P-value	Species
1	G188	7779802	5.20E-36	Lotus japonicus
1	G188	7284340	2.10E-34	Glycine max
1	G188	9361307	1.20E-27	Triticum aestivum
1	G188	7340336	1.10E-22	Oryza sativa
1	G188	6529152	3.60E-22	Lycopersicon esculentum
1	G188	8748477	7.70E-21	Medicago truncatula
1	G188	5456433	7.10E-14	Zea mays
1	G188	9302479	1.60E-12	Sorghum bicolor
1	G188	6696287	4.10E-12	Pinus taeda
1	G188	562242	9.00E-12	Brassica rapa
3	G616	7719440	8.30E-37	Lotus japonicus
3	G616	7692230	5.90E-33	Glycine max
3	G616	7501307	1.10E-21	Gossypium arboreum
3	G616	8071090	1.50E-21	Solanum tuberosum
3	G616	8858771	1.50E-21	Oryza sativa
3	G616	5047315	1.50E-21	Gossypium hirsutum
3	G616	6358532	5.80E-20	Antirrhinum graniticum
3	G616	2826867	7.00E-20	Antirrhinum majus
3	G616	6358535	7.40E-20	Antirrhinum majus subsp. linkianum
3	G616	6358538	7.50E-20	Antirrhinum braun-blauquetii
5	G19	8789223	2.80E-34	Citrus x paradisi
5	G19	9434234	4.50E-34	Lycopersicon esculentum
5	G19	7478682	1.30E-30	Glycine max
5	G19	6654934	1.20E-28	Medicago truncatula
5	G19	3264766	5.50E-26	Prunus armeniaca
5	G19	7624302	8.30E-26	Gossypium arboreum
5	G19	9425363	2.90E-25	Triticum aestivum
5	G19	688579	3.60E-25	Ricinus communis
5	G19	9419304	6.00E-25	Hordeum vulgare
5	G19	7720316	8.80E-25	Lotus japonicus
7	G261	5821137	5.10E-93	Nicotiana tabacum
7	G261	7158881	8.80E-86	Medicago sativa
7	G261	886741	1.00E-73	Zea mays
7	G261	5900449	5.20E-47	Lycopersicon esculentum
7	G261	7561318	1.20E-46	Medicago truncatula
7	G261	19491	1.70E-42	Lycopersicon peruvianum
7	G261	7233914	3.50E-41	Glycine max
7	G261	4528238	9.00E-41	Citrus unshiu
7	G261	8903922	4.00E-39	Hordeum vulgare
7	G261	9251913	1.90E-36	Solanum tuberosum
9	G28	7528275	4.20E-62	Mesembryanthemum crystallinum
9	G28	6654776	1.20E-57	Medicago truncatula
9	G28	790362	2.30E-54	Nicotiana tabacum
9	G28	8809570	8.00E-54	Nicotiana glauca
9	G28	3342210	8.40E-54	Lycopersicon esculentum
9	G28	6566281	8.40E-47	Glycine max
9	G28	7627061	8.40E-47	Gossypium arboreum
9	G28	7324479	2.00E-44	Lycopersicon pennellii
9	G28	6478844	1.80E-35	Matricaria chamomilla
9	G28	7273972	7.80E-29	Oryza sativa
11	G869	2213784	1.30E-19	Lycopersicon esculentum
11	G869	3065894	7.30E-19	Nicotiana tabacum

Figure 3B

SEQ ID No.	GID	Genbank NID	P-value	Species
11	G869	8570080	4.20E-18	Oryza sativa
11	G869	7560260	1.50E-17	Medicago truncatula
11	G869	7534890	5.20E-14	Sorghum bicolor
11	G869	6455322	1.10E-13	Glycine max
11	G869	9362061	2.70E-13	Triticum aestivum
11	G869	7788764	5.70E-13	Lotus japonicus
11	G869	7624302	2.50E-12	Gossypium arboreum
11	G869	3858036	2.80E-12	Populus balsamifera subsp. trichocarpa
13	G237	8283916	4.70E-42	Glycine max
13	G237	9361969	8.30E-41	Triticum aestivum
13	G237	4753385	4.10E-39	Zea mays
13	G237	7535969	4.10E-33	Sorghum bicolor
13	G237	7566043	9.30E-33	Medicago truncatula
13	G237	7339127	2.00E-32	Lycopersicon esculentum
13	G237	5860031	1.10E-28	Pinus taeda
13	G237	7776223	2.20E-28	Lotus japonicus
13	G237	6850206	5.10E-28	Oryza sativa
13	G237	5048991	8.50E-28	Gossypium hirsutum
15	G409	6654773	6.10E-57	Medicago truncatula
15	G409	6531235	2.00E-56	Lycopersicon esculentum
15	G409	7924152	1.10E-47	Glycine max
15	G409	5006854	6.50E-43	Oryza sativa
15	G409	8098529	2.10E-41	Hordeum vulgare
15	G409	767697	1.40E-37	Daucus carota
15	G409	8328991	3.30E-37	Mesembryanthemum crystallinum
15	G409	7415613	1.40E-32	Physcomitrella patens
15	G409	7785121	2.80E-32	Lotus japonicus
15	G409	6916941	4.80E-32	Lycopersicon pennellii
17	G418	7239156	1.90E-123	Malus x domestica
17	G418	5892190	2.00E-62	Lycopersicon esculentum
17	G418	7628137	8.70E-58	Gossypium arboreum
17	G418	9205496	3.90E-51	Glycine max
17	G418	6069643	1.50E-45	Oryza sativa
17	G418	7562931	6.90E-45	Medicago truncatula
17	G418	7781695	5.50E-40	Lotus japonicus
17	G418	9298824	7.80E-34	Sorghum bicolor
17	G418	9428023	3.90E-32	Triticum aestivum
17	G418	7244366	1.30E-31	Mentha x piperita
19	G591	7646333	1.90E-55	Lycopersicon esculentum
19	G591	7924288	4.10E-53	Glycine max
19	G591	7722838	1.10E-41	Lotus japonicus
19	G591	5804781	1.40E-24	Nicotiana tabacum
19	G591	9198126	2.50E-23	Medicago truncatula
19	G591	427677	9.50E-15	Oryza sativa
19	G591	7624745	1.80E-14	Gossypium arboreum
19	G591	7535578	8.70E-14	Sorghum bicolor
19	G591	5915205	1.30E-11	Zea mays
19	G591	9249806	2.60E-11	Solanum tuberosum
21	G525	4384535	5.60E-61	Lycopersicon esculentum
21	G525	6454868	2.00E-58	Glycine max
21	G525	6066594	9.30E-54	Petunia x hybrida
21	G525	4977542	8.60E-51	Oryza sativa

Figure 3C

SEQ ID No.	GID	Genbank NID	P-value	Species
21	G525	9361647	2.50E-50	Triticum aestivum
21	G525	4218536	5.20E-50	Triticum sp.
21	G525	6732159	5.20E-50	Triticum monococcum
21	G525	5343151	2.70E-49	Zea mays
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23	G545	7228328	3.70E-52	Medicago sativa
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23	G545	439492	3.90E-39	Petunia x hybrida
23	G545	4382658	1.70E-38	Lycopersicon esculentum
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23	G545	7322653	6.80E-37	Lycopersicon hirsutum
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25	G865	9417297	1.70E-32	Triticum aestivum
25	G865	7206394	4.90E-29	Medicago truncatula
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25	G865	790362	8.40E-22	Nicotiana tabacum
25	G865	7528275	5.90E-21	Mesembryanthemum crystallinum
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27	G881	8440065	1.00E-27	Gossypium hirsutum
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27	G881	9199620	2.70E-27	Medicago truncatula
27	G881	6472584	2.20E-24	Nicotiana tabacum
27	G881	9250698	3.20E-24	Solanum tuberosum
27	G881	8205146	5.20E-21	Oryza sativa
27	G881	1159878	8.20E-17	Avena fatua
27	G881	9299778	2.70E-16	Sorghum bicolor
27	G881	9444636	1.10E-14	Triticum aestivum
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29	G896	7628908	3.60E-82	Gossypium arboreum
29	G896	7244408	1.80E-79	Mentha x piperita
29	G896	5046180	2.10E-73	Gossypium hirsutum
29	G896	7678652	1.10E-63	Lotus japonicus
29	G896	8286031	1.40E-60	Glycine max
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29	G896	9298238	9.20E-54	Sorghum bicolor
29	G896	7566414	8.00E-52	Medicago truncatula
29	G896	8845076	1.00E-46	Triticum aestivum
31	G378	5270028	5.10E-73	Lycopersicon esculentum
31	G378	5048335	4.10E-58	Gossypium hirsutum
31	G378	7239521	5.90E-42	Oryza sativa
31	G378	5606120	6.80E-36	Glycine max
31	G378	3853800	3.20E-30	Populus tremula x Populus tremuloides
31	G378	7659983	1.70E-23	Sorghum bicolor

Figure 3D

SEQ ID No.	GID	Genbank NID	P-value	Species
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31	G378	3242033	4.30E-17	Mesembryanthemum crystallinum
31	G378	7626259	7.70E-13	Gossypium arboreum
33	G229	7337390	6.60E-51	Lycopersicon esculentum
33	G229	9823237	3.60E-50	Hordeum vulgare
33	G229	7244424	4.90E-50	Mentha x piperita
33	G229	7776053	1.70E-49	Lotus japonicus
33	G229	2921335	5.80E-48	Gossypium hirsutum
33	G229	1491932	4.50E-47	Zea mays
33	G229	6455590	2.80E-44	Glycine max
33	G229	6020191	2.00E-41	Pinus taeda
33	G229	10697236	4.20E-41	Oryza sativa
33	G229	7765706	5.10E-41	Medicago truncatula
35	G663	7673087	5.10E-43	Petunia integrifolia
35	G663	9508051	3.00E-41	Lycopersicon esculentum
35	G663	7673091	3.30E-41	Petunia x hybrida
35	G663	7673097	2.40E-36	Petunia axillaris
35	G663	5048991	1.20E-33	Gossypium hirsutum
35	G663	6455590	2.50E-31	Glycine max
35	G663	7560175	1.90E-27	Medicago truncatula
35	G663	7244424	4.10E-26	Mentha x piperita
35	G663	9954117	3.40E-25	Solanum tuberosum
35	G663	6020191	3.60E-25	Pinus taeda
37	G1396	498704	5.20E-22	Spinacia oleracea
37	G1396	7502400	1.20E-21	Gossypium arboreum
37	G1396	3857536	3.40E-21	Populus balsamifera subsp. trichocarpa
37	G1396	4385300	1.20E-20	Lycopersicon esculentum
37	G1396	6917249	1.50E-20	Lycopersicon pennellii
37	G1396	6915979	1.70E-20	Glycine max
37	G1396	7674530	2.70E-20	Medicago truncatula
37	G1396	8090319	3.40E-20	Sorghum bicolor
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37	G1396	6654124	1.10E-19	Zea mays
39	G265	5821137	6.50E-83	Nicotiana tabacum
39	G265	7158881	3.80E-79	Medicago sativa
39	G265	886741	1.60E-70	Zea mays
39	G265	5900449	5.60E-43	Lycopersicon esculentum
39	G265	8903922	8.20E-43	Hordeum vulgare
39	G265	7561318	2.10E-41	Medicago truncatula
39	G265	9204445	5.30E-36	Glycine max
39	G265	4528238	5.40E-36	Citrus unshiu
39	G265	19489	2.10E-35	Lycopersicon peruvianum
39	G265	9251913	2.00E-32	Solanum tuberosum
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41	G1006	3342210	4.90E-49	Lycopersicon esculentum
41	G1006	6654776	1.90E-48	Medicago truncatula
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41	G1006	8809570	2.00E-46	Nicotiana glauca
41	G1006	7627061	6.40E-41	Gossypium arboreum
41	G1006	7324479	1.20E-35	Lycopersicon pennellii
41	G1006	6478844	1.80E-35	Matricaria chamomilla

Figure 3E

SEQ ID No.	GID	Genbank NID	P-value	Species
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43	G1309	7566043	9.60E-35	Medicago truncatula
43	G1309	5891104	2.20E-31	Lycopersicon esculentum
43	G1309	5860031	2.10E-30	Pinus taeda
43	G1309	5049507	6.20E-30	Gossypium hirsutum
43	G1309	5139805	1.30E-29	Glycine max
43	G1309	6850206	2.50E-29	Oryza sativa
43	G1309	7721017	3.40E-29	Lotus japonicus
43	G1309	8368245	5.20E-28	Zea mays
43	G1309	20560	9.50E-27	Petunia x hybrida
45	G2550	4380729	2.80E-51	Lycopersicon esculentum
45	G2550	5667196	2.20E-49	Oryza sativa
45	G2550	8669454	1.40E-48	Glycine max
45	G2550	9298824	1.50E-48	Sorghum bicolor
45	G2550	7239156	9.90E-46	Malus x domestica
45	G2550	7570704	5.70E-45	Medicago truncatula
45	G2550	7628137	3.30E-42	Gossypium arboreum
45	G2550	7244366	6.00E-41	Mentha x piperita
45	G2550	9428023	4.70E-40	Triticum aestivum
45	G2550	9250642	3.50E-39	Solanum tuberosum
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47	G965	5892190	2.00E-62	Lycopersicon esculentum
47	G965	7628137	1.60E-56	Gossypium arboreum
47	G965	9205496	2.60E-49	Glycine max
47	G965	6069643	1.70E-45	Oryza sativa
47	G965	7562931	2.50E-44	Medicago truncatula
47	G965	7781695	1.60E-41	Lotus japonicus
47	G965	9298824	6.30E-33	Sorghum bicolor
47	G965	9428023	1.50E-31	Triticum aestivum
47	G965	7244366	1.20E-29	Mentha x piperita
49	G793	6976712	3.60E-43	Lycopersicon esculentum
49	G793	7924288	2.00E-41	Glycine max
49	G793	7614163	3.90E-34	Lotus japonicus
49	G793	9198126	5.70E-23	Medicago truncatula
49	G793	5804781	1.10E-22	Nicotiana tabacum
49	G793	7535578	1.60E-14	Sorghum bicolor
49	G793	427677	6.10E-14	Oryza sativa
49	G793	5915205	2.90E-10	Zea mays
49	G793	9249806	4.20E-10	Solanum tuberosum
49	G793	7624745	1.30E-09	Gossypium arboreum
51	G764	4384535	7.00E-70	Lycopersicon esculentum
51	G764	5049217	1.80E-65	Gossypium hirsutum
51	G764	6454868	1.90E-64	Glycine max
51	G764	6066594	5.20E-59	Petunia x hybrida
51	G764	4218536	2.30E-52	Triticum sp.
51	G764	6732159	2.30E-52	Triticum monococcum
51	G764	9361647	7.50E-52	Triticum aestivum
51	G764	4977542	4.10E-49	Oryza sativa
51	G764	6799764	4.40E-49	Medicago truncatula
51	G764	9296257	1.00E-48	Sorghum bicolor

Figure 3F

SEQ ID No.	GID	Genbank NID	P-value	Species
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53	G350	4666359	3.10E-48	Datisca glomerata
53	G350	1763062	8.30E-48	Glycine max
53	G350	7626808	9.10E-44	Gossypium arboreum
53	G350	7206360	2.20E-43	Medicago truncatula
53	G350	2981168	2.10E-38	Nicotiana tabacum
53	G350	7322653	2.00E-37	Lycopersicon hirsutum
53	G350	5276755	2.40E-37	Lycopersicon esculentum
53	G350	2058503	1.10E-31	Brassica rapa
55	G986	6472584	1.00E-34	Nicotiana tabacum
55	G986	8440065	8.80E-33	Gossypium hirsutum
55	G986	4385167	1.50E-32	Lycopersicon esculentum
55	G986	8205146	5.50E-30	Oryza sativa
55	G986	5820418	8.80E-26	Glycine max
55	G986	1159878	2.30E-23	Avena fatua
55	G986	9250698	4.60E-22	Solanum tuberosum
55	G986	9413507	7.90E-21	Triticum aestivum
55	G986	7748539	2.30E-20	Lotus japonicus
55	G986	9199620	1.30E-16	Medicago truncatula
57	G1349	8904043	1.50E-47	Hordeum vulgare
57	G1349	7244408	2.40E-47	Mentha x piperita
57	G1349	8286031	3.60E-46	Glycine max
57	G1349	9298238	9.10E-36	Sorghum bicolor
57	G1349	7628908	4.70E-34	Gossypium arboreum
57	G1349	5046180	1.50E-33	Gossypium hirsutum
57	G1349	5888938	1.30E-30	Lycopersicon esculentum
57	G1349	5043924	6.20E-30	Pinus taeda
57	G1349	8845076	4.40E-29	Triticum aestivum
57	G1349	7678652	4.20E-27	Lotus japonicus

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Ratcliffe, Oliver  
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cat cat cag cat caa gag ttt tca ttc gtt ccc gac cat ttg ata tca    890
His His Gln His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser
                240                245                250

ccg gca gaa tcc aac ggc gga gca ttc aat ctt gat ttt aat atg tca    938
Pro Ala Glu Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser
                255                260                265

aca ccc tcc ggc gcc gga gct gcc gtc tcc gcc gca tca ggt ggt ggc    986
Thr Pro Ser Gly Ala Gly Ala Val Ser Ala Ala Ser Gly Gly Gly
                275                280                285

ttc agt ggt ttc aac agg ggg acc ctt cag tcc aat tca aca aat cag    1034
Phe Ser Gly Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln
                290                295                300

cat cag tca ttc ctc gct aat cta cag agg ttt cca aca tca gaa agt    1082
His Gln Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser
                305                310                315

gga gga ggt cca cag ttc tta ttc ggt gca ctg cct gca gag aat cac    1130
Gly Gly Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His
                320                325                330

cac cac aat cac cag ttt cag ctt tac tat gaa aat gga tgc aga aac    1178
His His Asn His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn
                335                340                345                350

tca tca gaa cat aag ggt aaa ggc aag aac tga tgatattaat tattgcacat    1231
Ser Ser Glu His Lys Gly Lys Gly Lys Asn
                355                360

ttgggttttgt tcaaagtctc attttgtatg tttatctttg gtttatttca aaacaaatgt    1291

taatctctttt cggtgtctga tgtgtgttag gggtttgttt tatgtattga gggctcttgg    1351

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Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys  
35 40 45

Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln  
50 55 60

Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala  
65 70 75 80

## MBI15 Sequence Listing.ST25

Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Ser Glu Leu Pro  
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                     100                    105                    110  
 Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys  
                     115                    120                    125  
 Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Ser Gly Leu Ser Leu Ser  
                     130                    135                    140  
 Arg Ser Glu Leu Arg Asp Lys Ala Arg Glu Arg Ala Arg Glu Arg Thr  
                     145                    150                    155                    160  
 Ala Lys Glu Thr Lys Glu Arg Asp His Asn His Thr Ser Phe Thr Asp  
                     165                    170                    175  
 Leu Leu Asn Ser Gly Ser Asp Pro Val Asn Ser Asn Arg Gln Trp Met  
                     180                    185                    190  
 Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly Leu  
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 Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn Ser  
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 His Pro Phe Ser Ser Ile Ser Asp His His His His His Pro His His  
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 Gln His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala  
                     245                    250                    255  
 Glu Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro  
                     260                    265                    270  
 Ser Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser  
                     275                    280                    285  
 Gly Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln  
                     290                    295                    300  
 Ser Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly  
                     305                    310                    315                    320  
 Gly Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His  
                     325                    330                    335  
 Asn His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn Ser Ser  
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 acc aag gcc aag ggc cgt aaa ctc acg gct gag gaa ctc tgg tca gag 159  
 Thr Lys Ala Lys Gly Arg Lys Leu Thr Ala Glu Glu Leu Trp Ser Glu  
           15                          20                          25                          30  
 ctc gat gct tcc gcc gcc gac gac ttc tgg ggt ttc tat tcc acc tcc 207  
 Leu Asp Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser  
                           35                          40                          45  
 aaa ctc cat ccc acc aac caa gtt aac gtg aaa gag gag gca gtg aag 255  
 Lys Leu His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys  
                           50                          55                          60  
 aag gag cag gca aca gag ccg ggg aaa ccg agg aag agg aag aat gtt 303  
 Lys Glu Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val  
                           65                          70                          75  
 tat aga ggg ata cgt aag cgt cca tgg gga aaa tgg gcg gct gag att 351  
 Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile  
           80                          85                          90  
 cga gat cca cga aaa ggt gtt aga gtt tgg ctt ggt acg ttc aac acg 399  
 Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr  
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 gcg gag gaa gct gcc atg gct tat gat gtt gcg gcc aag cag atc cgt 447  
 Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg  
                           115                          120                          125  
 ggt gat aaa gcc aag ctc aac ttc cca gat ctg cac cat cct cct cct 495  
 Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro  
                           130                          135                          140  
 cct aat tat act cct ccg ccg tca tcg cca cga tca acc gat cag cct 543  
 Pro Asn Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro  
                           145                          150                          155  
 ccg gcg aag aag gtc tgc gtt gtc tct cag agt gag agc gag tta agt 591  
 Pro Ala Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser  
           160                          165                          170  
 cag ccg agt ttc ccg gtg gag tgt ata gga ttt gga aat ggg gac gag 639  
 Gln Pro Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu  
           175                          180                          185                          190  
 ttt cag aac ctg agt tac gga ttt gag ccg gat tat gat ctg aaa cag 687  
 Phe Gln Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln  
                           195                          200                          205  
 cag ata tcg agc ttg gaa tcg ttc ctt gag ctg gac ggt aac acg gcg 735  
 Gln Ile Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala  
                           210                          215                          220  
 gag caa ccg agt cag ctt gat gag tcc gtt tcc gag gtg gat atg tgg 783  
 Glu Gln Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp  
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 atg ctt gat gat gtc att gcg tcg tat gag taa aagaaaaaa ataagtttaa 836  
 Met Leu Asp Asp Val Ile Ala Ser Tyr Glu

## MBI15 Sequence Listing.ST25

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aaaaagttaa ataaagtctg taatatatat gtaaccgccg ttacttttaa aaggttttta 896  
ccgtcgcatc ggactgctga tgatgtctgt tgtgtaatgt gtagaatgtg accaaatgga 956  
cgttatatta cggtttgtgg tattattagt ttcttagatg gaaaaactta catgtgtaaa 1016  
taagatttgt aatgtaagac gaagtactta taacttctt 1055

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20 25 30

Ala Ser Ala Ala Asp Asp Phe Trp Gly Phe Tyr Ser Thr Ser Lys Leu  
35 40 45

His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu  
50 55 60

Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg  
65 70 75 80

Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp  
85 90 95

Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu  
100 105 110

Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp  
115 120 125

Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn  
130 135 140

Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala  
145 150 155 160

Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro  
165 170 175

Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln  
180 185 190

Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile  
195 200 205

Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln  
210 215 220

Pro Ser Gln Leu Asp Glu Ser Val Ser Glu Val Asp Met Trp Met Leu

## MBI15 Sequence Listing.ST25

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230

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Asp Asp Val Ile Ala Ser Tyr Glu  
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gcttttgctt gattgtcttt tatttagaaa cagtggtagag tttttagtct ttcactttgt 180  
tcaagttcga agcttttttt ggaggggaatt ttgggcttct gattttgatc gaaacttact 240  
gatagtaagt tctttgagtc ctcccttaact gtagtttctg tgtactgaag ttattgaatt 300  
gaaagttttt atcttttttg gttattgaaa ctttcatagt ttgatcaaaa gagtctcttg 360  
ctctgttttt ggctctgttt ttgtgagtgt gattgtaagc tttgttgtga gtagattgaa 420  
tcaaggagtg tgagagttgt taaaagtgtt ttcagag atg gat gag aat aat cat 475  
Met Asp Glu Asn Asn His  
1 5  
gga gtt tca tca agc tca ctt cca cct ttc ctc acc aaa aca tat gag 523  
Gly Val Ser Ser Ser Ser Leu Pro Pro Phe Leu Thr Lys Thr Tyr Glu  
10 15 20  
atg gtt gat gat tct tca tcc gat tct atc gtc tct tgg agt cag agc 571  
Met Val Asp Asp Ser Ser Ser Asp Ser Ile Val Ser Trp Ser Gln Ser  
25 30 35  
aat aag agt ttc atc gtt tgg aat ccg ccg gag ttt tct aga gat ctt 619  
Asn Lys Ser Phe Ile Val Trp Asn Pro Pro Glu Phe Ser Arg Asp Leu  
40 45 50  
ctt ccg aga ttc ttc aag cac aat aac ttc tct agc ttt atc cgc cag 667  
Leu Pro Arg Phe Phe His His Asn Asn Phe Ser Ser Phe Ile Arg Gln  
55 60 65 70  
ctt aac aca tat ggt ttt aga aaa gct gat cct gag caa tgg gaa ttt 715  
Leu Asn Thr Tyr Gly Phe Arg Lys Ala Asp Pro Glu Gln Trp Glu Phe  
75 80 85  
gcg aat gat gat ttt gtg aga ggt caa cct cat ctt atg aag aac att 763  
Ala Asn Asp Asp Phe Val Arg Gly Gln Pro His Leu Met Lys Asn Ile  
90 95 100  
cat aga cgc aaa cca gtt cat agc cac tct tta ccg aat ctt caa gct 811  
His Arg Arg Lys Pro Val His Ser His Ser Leu Pro Asn Leu Gln Ala  
105 110 115  
cag tta aac ccg ttg acg gat tca gaa cga gtg aga atg aat aat cag 859  
Gln Leu Asn Pro Leu Thr Asp Ser Glu Arg Val Arg Met Asn Asn Gln  
120 125 130  
att gag aga ttg aca aaa gag aaa gaa gga ttg ctt gaa gag tta cat 907  
Ile Glu Arg Leu Thr Lys Glu Lys Glu Gly Leu Leu Glu Glu Leu His  
135 140 145 150  
aaa caa gac gag gaa cga gaa gtg ttt gag atg caa gtg aaa gaa ctt 955  
Lys Gln Asp Glu Glu Arg Glu Val Phe Glu Met Gln Val Lys Glu Leu

MBI15 Sequence Listing.ST25

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	170	175	
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	185	190	
ccg tgt gtt ccc gaa aca aac gag agg aaa aga agg ttc cct agg atc Pro Cys Val Pro Glu Thr Asn Glu Arg Lys Arg Arg Phe Pro Arg Ile			1099
	200	205	
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	215	220	
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	235	240	
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	250	255	
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	265	270	
ctt gat gtg gat gaa tca tct act ttt cca gag agc cct cct ctt tct Leu Asp Val Asp Glu Ser Ser Thr Phe Pro Glu Ser Pro Pro Leu Ser			1339
	280	285	
tgc ata cag tta agt gtc gat tca cgt ctc aaa tct cct cct tct cca Cys Ile Gln Leu Ser Val Asp Ser Arg Leu Lys Ser Pro Pro Ser Pro			1387
	295	300	
agg atc atc gat atg aac tgt gag ccc gat ggt tcg aaa gaa cag aac Arg Ile Ile Asp Met Asn Cys Glu Pro Asp Gly Ser Lys Glu Gln Asn			1435
	315	320	
act gtt gct gct cct cct cct cct cca gta gca gga gcg aat gat ggc Thr Val Ala Ala Pro Pro Pro Pro Pro Val Ala Gly Ala Asn Asp Gly			1483
	330	335	
ttc tgg cag cag ttt ttc tca gag aat cct ggc tca acc gag caa cgg Phe Trp Gln Gln Phe Phe Ser Glu Asn Pro Gly Ser Thr Glu Gln Arg			1531
	345	350	
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	360	365	
act gag aaa tgt tgg tgg aat tcg aga aat gtt aat gca att aca gaa Thr Glu Lys Cys Trp Trp Asn Ser Arg Asn Val Asn Ala Ile Thr Glu			1627
	375	380	
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	395	400	
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cgattccagt acttaggtat ggttcagctg tttatattatc acttgatga tctttcccag			1793
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aaaa			1857

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Val Ser Trp Ser Gln Ser Asn Lys Ser Phe Ile Val Trp Asn Pro Pro
35          40          45

Glu Phe Ser Arg Asp Leu Leu Pro Arg Phe Phe Lys His Asn Asn Phe
50          55          60

Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ala Asp
65          70          75          80

Pro Glu Gln Trp Glu Phe Ala Asn Asp Asp Phe Val Arg Gly Gln Pro
85          90          95

His Leu Met Lys Asn Ile His Arg Arg Lys Pro Val His Ser His Ser
100         105         110

Leu Pro Asn Leu Gln Ala Gln Leu Asn Pro Leu Thr Asp Ser Glu Arg
115         120         125

Val Arg Met Asn Asn Gln Ile Glu Arg Leu Thr Lys Glu Lys Glu Gly
130         135         140

Leu Leu Glu Glu Leu His Lys Gln Asp Glu Glu Arg Glu Val Phe Glu
145         150         155         160

Met Gln Val Lys Glu Leu Lys Glu Arg Leu Gln His Met Glu Lys Arg
165         170         175

Gln Lys Thr Met Val Ser Phe Val Ser Gln Val Leu Glu Lys Pro Gly
180         185         190

Leu Ala Leu Asn Leu Ser Pro Cys Val Pro Glu Thr Asn Glu Arg Lys
195         200         205

Arg Arg Phe Pro Arg Ile Glu Phe Phe Pro Asp Glu Pro Met Leu Glu
210         215         220

Glu Asn Lys Thr Cys Val Val Val Arg Glu Glu Gly Ser Thr Ser Pro
225         230         235         240

Ser Ser His Thr Arg Glu His Gln Val Glu Gln Leu Glu Ser Ser Ile
245         250         255

Ala Ile Trp Glu Asn Leu Val Ser Asp Ser Cys Glu Ser Met Leu Gln
260         265         270

Ser Arg Ser Met Met Thr Leu Asp Val Asp Glu Ser Ser Thr Phe Pro
275         280         285

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MBI15 Sequence Listing.ST25

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Lys Ser Pro Pro Ser Pro Arg Ile Ile Asp Met Asn Cys Glu Pro Asp  
 305 310 315 320

Gly Ser Lys Glu Gln Asn Thr Val Ala Ala Pro Pro Pro Pro Val  
 325 330 335

Ala Gly Ala Asn Asp Gly Phe Trp Gln Gln Phe Phe Ser Glu Asn Pro  
 340 345 350

Gly Ser Thr Glu Gln Arg Glu Val Gln Leu Glu Arg Lys Asp Asp Lys  
 355 360 365

Asp Lys Ala Gly Val Arg Thr Glu Lys Cys Trp Trp Asn Ser Arg Asn  
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Ser

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 Met Ser Met Thr Ala Asp Ser Gln Ser Asp Tyr Ala Phe Leu Glu  
 1 5 10 15  
 tcc ata cga cga cac tta cta gga gaa tcg gag ccg ata ctc agt gag 155  
 Ser Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu  
 20 25 30  
 tcg aca gcg agt tcg gtt act caa tct tgt gta acc ggt cag agc att 203  
 Ser Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile  
 35 40 45  
 aaa ccg gtg tac gga cga aac cct agc ttt agc aaa ctg tat cct tgc 251  
 Lys Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys  
 50 55 60  
 ttc acc gag agc tgg gga gat ttg ccg ttg aaa gaa aac gat tct gag 299  
 Phe Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu  
 65 70 75  
 gat atg tta gtt tac ggt atc ctc aac gac gcc ttt cac ggc ggt tgg 347  
 Asp Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp  
 80 85 90 95  
 gag ccg tct tct tcg tct tcc gac gaa gat cgt agc tct ttc ccg agt 395  
 Glu Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser  
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MBI15 Sequence Listing.ST25

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Val Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala	
130 135 140	
aag gga aag cat tat aga gga gtg aga caa agg ccg tgg ggg aaa ttt	539
Lys Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe	
145 150 155	
gcg gcg gag att aga gat ccg gcg aag aac gga gct agg gtt tgg tta	587
Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu	
160 165 170 175	
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Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala	
180 185 190	
gct ttc agg atg cgt ggt tcc cgc gct ttg ttg aat ttt ccg ttg aga	683
Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg	
195 200 205	
gtt aat tca gga gaa ccc gac ccg gtt cga atc aag tcc aag aga tct	731
Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser	
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tct ttt tct tct tct aac gag aac gga gct ccg aag aag agg aga acg	779
Ser Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr	
225 230 235	
gtg gcc gcc ggt ggt gga atg gat aag gga ttg acg gtg aag tgc gag	827
Val Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu	
240 245 250 255	
gtt gtt gaa gtg gca cgt ggc gat cgt tta ttg gtt tta taa	869
Val Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu	
260 265	
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aaaattcggtt tattattataa aaaaaaaaaa aaaaa	964

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35 40 45	
Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe	
50 55 60	
Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp	
65 70 75 80	
Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu	
85 90 95	

Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser Val

Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala Lys  
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Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly  
165 170 175

Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val  
195 200 205

Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser  
210 215 220

Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val  
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<223> G869
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[illegible]

## MBI15 Sequence Listing.ST25

Ser 15	Glu	Ile	Lys	Lys	Arg 20	Ala	Lys	Arg	Asn	Thr 25	Leu	Ser	Ser	Leu	Pro 30	
caa	gaa	acc	caa	cct	ttg	agg	aaa	gtc	cgt	att	att	gtg	aat	gat	cct	565
Gln	Glu	Thr	Gln	Pro	Leu	Arg	Lys	Val	Arg	Ile	Ile	Val	Asn	Asp	Pro	
				35				40					45			
tat	gct	act	gat	gat	tcc	tct	agt	gat	gag	gaa	gag	ctt	aag	gtt	cct	613
Tyr	Ala	Thr	Asp	Asp	Ser	Ser	Ser	Asp	Glu	Glu	Glu	Leu	Lys	Val	Pro	
			50				55					60				
aag	cca	agg	aaa	atg	aaa	cgt	atc	gtt	cgt	gag	att	aac	ttt	cct	tct	661
Lys	Pro	Arg	Lys	Met	Lys	Arg	Ile	Val	Arg	Glu	Ile	Asn	Phe	Pro	Ser	
		65				70					75					
atg	gaa	gtt	tct	gaa	cag	cct	tct	gag	agt	tct	tct	cag	gac	agt	act	709
Met	Glu	Val	Ser	Glu	Gln	Pro	Ser	Glu	Ser	Ser	Ser	Gln	Asp	Ser	Thr	
	80					85					90					
aaa	act	gat	ggc	aag	ata	gct	gtg	tca	gct	tct	cct	gct	gtt	cct	agg	757
Lys	Thr	Asp	Gly	Lys	Ile	Ala	Val	Ser	Ala	Ser	Pro	Ala	Val	Pro	Arg	
	95				100					105					110	
aag	aag	cct	gtt	ggc	gtt	agg	caa	agg	aaa	tgg	ggg	aaa	tgg	gct	gct	805
Lys	Lys	Pro	Val	Gly	Val	Arg	Gln	Arg	Lys	Trp	Gly	Lys	Trp	Ala	Ala	
				115				120						125		
gag	att	aga	gat	cct	att	aag	aaa	act	agg	act	tgg	ttg	ggc	act	ttt	853
Glu	Ile	Arg	Asp	Pro	Ile	Lys	Lys	Thr	Arg	Thr	Trp	Leu	Gly	Thr	Phe	
			130					135					140			
gat	act	ctt	gaa	gaa	gct	gct	aaa	gct	tat	gat	gct	aag	aag	ctt	gat	901
Asp	Thr	Leu	Glu	Glu	Ala	Ala	Lys	Ala	Tyr	Asp	Ala	Lys	Lys	Leu	Glu	
			145				150					155				
ttt	gat	gct	att	gtt	gct	gga	aat	gtg	tcc	act	act	aaa	cgt	gat	gtt	949
Phe	Asp	Ala	Ile	Val	Ala	Gly	Asn	Val	Ser	Thr	Thr	Lys	Arg	Asp	Val	
	160					165					170					
tct	tca	tct	gag	act	agc	caa	tgc	tct	cgt	tct	tca	cct	gtt	gtt	cct	997
Ser	Ser	Ser	Glu	Thr	Ser	Gln	Cys	Ser	Arg	Ser	Ser	Pro	Val	Val	Pro	
	175				180					185					190	
gtt	gag	caa	gat	gac	act	tct	gca	tca	gct	ctc	act	tgt	gtc	aac	aac	1045
Val	Glu	Gln	Asp	Asp	Thr	Ser	Ala	Ser	Ala	Leu	Thr	Cys	Val	Asn	Asn	
				195				200						205		
cct	gat	gac	gtc	tgc	acc	gtt	gct	cca	act	gct	cca	act	cca	aat	gtt	1093
Pro	Asp	Asp	Val	Ser	Thr	Val	Ala	Pro	Thr	Ala	Pro	Thr	Pro	Asn	Val	
			210					215					220			
cct	gct	ggc	gga	aac	aag	gaa	acg	ttg	ttc	gat	ttc	gac	ttt	act	aat	1141
Pro	Ala	Gly	Gly	Asn	Lys	Glu	Thr	Leu	Phe	Asp	Phe	Asp	Phe	Thr	Asn	
		225					230					235				
cta	cag	atc	cct	gat	ttt	ggc	ttc	ttg	gca	gag	gag	caa	caa	gac	cta	1189
Leu	Gln	Ile	Pro	Asp	Phe	Gly	Phe	Leu	Ala	Glu	Glu	Gln	Gln	Asp	Leu	
	240					245					250					
gac	ttc	gat	tgt	ttc	ctc	gcg	gat	gat	cag	ttt	gat	gat	ttc	ggc	ttg	1237
Asp	Phe	Asp	Cys	Phe	Leu	Ala	Asp	Asp	Gln	Phe	Asp	Asp	Phe	Gly	Leu	
	255				260					265					270	
ctt	gat	gac	att	caa	gga	ttc	gaa	gat	aac	ggc	cca	agt	gcg	tta	cca	1285
Leu	Asp	Asp	Ile	Gln	Gly	Phe	Glu	Asp	Asn	Gly	Pro	Ser	Ala	Leu	Pro	
				275				280						285		
gat	ttc	gac	ttt	gcg	gat	gtt	gaa	gat	ctt	cag	cta	gct	gac	tct	agt	1333
Asp	Phe	Asp	Phe	Ala	Asp	Val	Glu	Asp	Leu	Gln	Leu	Ala	Asp	Ser	Ser	
			290					295					300			
ttc	ggc	ttc	ctt	gat	caa	ctt	gct	cct	atc	aac	atc	tct	tgc	cca	tta	1381
Phe	Gly	Phe	Leu	Asp	Gln	Leu	Ala	Pro	Ile	Asn	Ile	Ser	Cys	Pro	Leu	
		305					310						315			

## MBI15 Sequence Listing.ST25

aaa agt ttt gca gct tca tag gatcttgctt agtaatgtta agtgagaaga 1432  
 Lys Ser Phe Ala Ala Ser  
 320

gtgttttggt ttttcgttta tgcttttagta atttaagaca tacaaaagtg tgtgttccgg 1492

attgtagtaa gatcttaaga cataaagccg ggttttgcaa ttaggaatcg agttttaatg 1552

aagttttagt ttatgtttg 1571

<210> 12

<211> 324

<212> PRT

<213> Arabidopsis thaliana

<400> 12

Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser Ser Glu  
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Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro Gln Glu  
 20 25 30

Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro Tyr Ala  
 35 40 45

Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro  
 50 55 60

Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser Met Glu  
 65 70 75 80

Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr  
 85 90 95

Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys  
 100 105 110

Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala Glu Ile  
 115 120 125

Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe Asp Thr  
 130 135 140

Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu Phe Asp  
 145 150 155 160

Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser  
 165 170 175

Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu  
 180 185 190

Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp  
 195 200 205

Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala  
 210 215 220

Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln

MBI15 Sequence Listing.ST25

225	230	235	240
Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe	245	250	255
Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp	260	265	270
Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe	275	280	285
Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly	290	295	300
Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu Lys Ser	305	310	315
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Phe Ala Ala Ser			

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 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(852)  
 <223> G237

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		1 5 10 15	
		cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat	96
		Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His	
		20 25 30	
		tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg	144
		Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly	
		35 40 45	
		aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag	192
		Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys	
		50 55 60	
		agg gat atg att agt gca gaa gaa gaa gag act atc ttg acg ttt cat	240
		Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His	
		65 70 75 80	
		tct ccc ttg ggt aac aag tgg tcg caa ata gct aaa ttc tta ccg gga	288
		Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly	
		85 90 95	
		aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag	336
		Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys	
		100 105 110	
		aaa tgg ctc aag tct cag agc tta caa gat gca aaa tct att tcc cct	384
		Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro	
		115 120 125	
		cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg	432
		Pro Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro	
		130 135 140	

MBI15 Sequence Listing.ST25

gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu 145 150 155 160	480
aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His 165 170 175	528
caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp 180 185 190	576
ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp 195 200 205	624
tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr 210 215 220	672
gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile 225 230 235 240	720
aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys 245 250 255	768
aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser 260 265 270	816
tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr 275 280	862
ttgtaatgta aatcaaattt ctaaggcaaa accggaaaaa aaaaaaaaaa aaaaaaaaaa	920

<210> 14  
 <211> 283  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 14

Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser 1 5 10 15
Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His 20 25 30
Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly 35 40 45
Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys 50 55 60
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His 65 70 75 80
Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly 85 90 95
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys 100 105 110
Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro

MBI15 Sequence Listing.ST25

115	120	125
Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro		
130	135	140
Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu		
145	150	155
Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His		
165	170	175
Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp		
180	185	190
Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp		
195	200	205
Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr		
210	215	220
Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile		
225	230	235
Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys		
245	250	255
Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser		
260	265	270
Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr		
275	280	

<210> 15  
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 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <223> G409

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atgatgggat tttgtatctg cccgttgag tcacctgcga gattactatg gattacaagc	180
ttcttcgcc ataagatcat gatcttctaa tccttctac ttcttcccat ctttttaatc	240
atcttctcgc tatctctgct tcctctttct ctctgtttcc tctttctcag aactcagaag	300
tagttgttgt tttatttctg ttgatcaaaa atg gaa tcc aat tcg ttt ttc ttc	354
Met Glu Ser Asn Ser Phe Phe Phe	
1 5	
gat cca tct gct tca cac ggc aac agc atg ttc ttc ctt ggg aat ctc	402
Asp Pro Ser Ala Ser His Gly Asn Ser Met Phe Phe Leu Gly Asn Leu	
10 15 20	
aat ccc gtc gtc caa gga gga gga gca aga tcg atg atg aac atg gag	450
Asn Pro Val Val Gln Gly Gly Gly Ala Arg Ser Met Met Asn Met Glu	

MBI15 Sequence Listing.ST25

25	30	35	40	
gaa act tcg aag cga agg ccc ttc ttt agc tcc cct gag gat ctc tac				498
Glu Thr Ser Lys Arg Arg Pro Phe Phe Ser Ser Pro Glu Asp Leu Tyr	45	50	55	
gac gat gac ttt tac gac gac cag ttg cct gaa aag aag cgt cgc ctc				546
Asp Asp Asp Phe Tyr Asp Asp Gln Leu Pro Glu Lys Lys Arg Arg Leu	60	65	70	
act acc gaa caa gtg cat ctg ctg gag aaa agc ttc gag aca gag aac				594
Thr Thr Glu Gln Val His Leu Leu Glu Lys Ser Phe Glu Thr Glu Asn	75	80	85	
aag cta gag cct gaa cgc aag act cag ctt gcc aag aag ctt ggt cta				642
Lys Leu Glu Pro Glu Arg Lys Thr Gln Leu Ala Lys Lys Leu Gly Leu	90	95	100	
cag cca agg caa gtg gct gtc tgg ttt cag aat cgc cga gct cgt tgg				690
Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp	105	110	115	120
aaa aca aaa cag ctt gag aga gac tac gat ctt ctc aag tcc act tac				738
Lys Thr Lys Gln Leu Glu Arg Asp Tyr Asp Leu Leu Lys Ser Thr Tyr	125	130	135	
gac caa ctt ctt tct aac tac gac tcc atc gtc atg gac aac gat aag				786
Asp Gln Leu Leu Ser Asn Tyr Asp Ser Ile Val Met Asp Asn Asp Lys	140	145	150	
ctc aga tcc gag gtt act tcc ctg acc gaa aag ctt cag ggc aaa caa				834
Leu Arg Ser Glu Val Thr Ser Leu Thr Glu Lys Leu Gln Gly Lys Gln	155	160	165	
gag aca gct aat gaa cca cct ggt caa gtg ccc gaa cca aac caa ctt				882
Glu Thr Ala Asn Glu Pro Pro Gly Gln Val Pro Glu Pro Asn Gln Leu	170	175	180	
gat ccg gtt tac att aat gcg gca gca atc aaa acc gag gac cgg tta				930
Asp Pro Val Tyr Ile Asn Ala Ala Ala Ile Lys Thr Glu Asp Arg Leu	185	190	195	200
agt tca ggg agc gtt ggg agc gcg gta cta gac gac gac gca cct caa				978
Ser Ser Gly Ser Val Gly Ser Ala Val Leu Asp Asp Asp Ala Pro Gln	205	210	215	
cta cta gac agc tgt gac tct tac ttc cca agc atc gta ccc atc caa				1026
Leu Leu Asp Ser Cys Asp Ser Tyr Phe Pro Ser Ile Val Pro Ile Gln	220	225	230	
gac aac agc aac gcc agt gat cat gac aat gac cgg agc tgt ttc gcc				1074
Asp Asn Ser Asn Ala Ser Asp His Asp Asn Asp Arg Ser Cys Phe Ala	235	240	245	
gac gtc ttt gtg ccc acc act tca ccg tcg cac gat cat cac ggt gaa				1122
Asp Val Phe Val Pro Thr Thr Ser Pro Ser His Asp His His Gly Glu	250	255	260	
tca ttg gct ttc tgg gga tgg cct tag aaaaccactc tgataataaa				1169
Ser Leu Ala Phe Trp Gly Trp Pro	265	270		
tggtgtgttta ttttaagttca agagtcattct tcttgttggt tccatgttga cgataattgt				1229
tgactcgtgg aataattccg ctgttcaacg gtatttttat cagttgcatt atatgctttt				1289
atgaaaaaaaa aaa				1302

<210> 16  
 <211> 272  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 16

## MBI15 Sequence Listing.ST25

Met Glu Ser Asn Ser Phe Phe Phe Asp Pro Ser Ala Ser His Gly Asn  
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Ser Met Phe Phe Leu Gly Asn Leu Asn Pro Val Val Gln Gly Gly Gly  
 20 25 30

Ala Arg Ser Met Met Asn Met Glu Glu Thr Ser Lys Arg Arg Pro Phe  
 35 40 45

Phe Ser Ser Pro Glu Asp Leu Tyr Asp Asp Asp Phe Tyr Asp Asp Gln  
 50 55 60

Leu Pro Glu Lys Lys Arg Arg Leu Thr Thr Glu Gln Val His Leu Leu  
 65 70 75 80

Glu Lys Ser Phe Glu Thr Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr  
 85 90 95

Gln Leu Ala Lys Lys Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp  
 100 105 110

Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Arg Asp  
 115 120 125

Tyr Asp Leu Leu Lys Ser Thr Tyr Asp Gln Leu Leu Ser Asn Tyr Asp  
 130 135 140

Ser Ile Val Met Asp Asn Asp Lys Leu Arg Ser Glu Val Thr Ser Leu  
 145 150 155 160

Thr Glu Lys Leu Gln Gly Lys Gln Glu Thr Ala Asn Glu Pro Pro Gly  
 165 170 175

Gln Val Pro Glu Pro Asn Gln Leu Asp Pro Val Tyr Ile Asn Ala Ala  
 180 185 190

Ala Ile Lys Thr Glu Asp Arg Leu Ser Ser Gly Ser Val Gly Ser Ala  
 195 200 205

Val Leu Asp Asp Asp Ala Pro Gln Leu Leu Asp Ser Cys Asp Ser Tyr  
 210 215 220

Phe Pro Ser Ile Val Pro Ile Gln Asp Asn Ser Asn Ala Ser Asp His  
 225 230 235 240

Asp Asn Asp Arg Ser Cys Phe Ala Asp Val Phe Val Pro Thr Thr Ser  
 245 250 255

Pro Ser His Asp His His Gly Glu Ser Leu Ala Phe Trp Gly Trp Pro  
 260 265 270

<210> 17  
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<223> G418

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gatattaaca	tatatcatga	agaaaaagat	tgaagtattg	at	atg gga ata act	114												
					Met Gly Ile Thr													
					1													
aaa act tct cct aat act aca att ctc ttg aag act ttt cac aat aat	162																	
Lys Thr Ser Pro Asn Thr Ile Leu Leu Lys Thr Phe His Asn Asn																		
5 10 20																		
tct atg tcc caa gat tat cat cat cat cat cat cat aat caa cac caa	210																	
Ser Met Ser Gln Asp Tyr His His His His His His Asn Gln His Gln																		
25 30 35																		
gga ggt atc ttc aac ttc tct aat gga ttc gac cga tca gat tct ccc	258																	
Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg Ser Asp Ser Pro																		
40 45 50																		
aat tta aca act cag cag aag caa gag cat caa agg gta gag atg gac	306																	
Asn Leu Thr Gln Gln Lys Gln Glu His Gln Arg Val Glu Met Asp																		
55 60 65																		
gag gaa tct tca gtc gcc gga ggt agg att ccg gtc tac gaa tca gcc	354																	
Glu Glu Ser Ser Val Ala Gly Gly Arg Ile Pro Val Tyr Glu Ser Ala																		
70 75 80																		
ggt atg tta tcc gaa atg ttt aat ttc ccc gga agc agc ggt gga gga	402																	
Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser Ser Gly Gly Gly																		
85 90 95 100																		
aga gat ctc gac ctc ggc caa tct ttc cgg tca aat agg cag ttg ctt	450																	
Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn Arg Gln Leu Leu																		
105 110 115																		
gag gag caa cat cag aat att ccg gct atg aat gct acg gat tca gcc	498																	
Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala Thr Asp Ser Ala																		
120 125 130																		
acc gcc acc gca gcc gcc atg cag tta ttc ttg atg aat cca ccg cca	546																	
Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met Asn Pro Pro Pro																		
135 140 145																		
ccg caa caa cca ccg tct ccg tca tcc aca act tcc cca agg agc cac	594																	
Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser Pro Arg Ser His																		
150 155 160																		
cac aat tct tca act ctt cac atg tta ctt cca agt cca tcc acc aac	642																	
His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser Pro Ser Thr Asn																		
165 170 175 180																		
aca act cac cat cag aac tac act aat cat atg tct atg cat cag ctt	690																	
Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser Met His Gln Leu																		
185 190 195																		
cca cat cag cat cac caa cag ata tcg acg tgg cag tct tct ccc gat	738																	
Pro His Gln His His Gln Gln Ile Ser Thr Trp Gln Ser Ser Pro Asp																		
200 205 210																		
cat cat cat cat cat cac aac agc caa acg gag att ggg acc gtc cac	786																	
His His His His His Asn Ser Gln Thr Glu Ile Gly Thr Val His																		
215 220 225																		
gtg gaa aac agc gga gga cac gga gga caa ggc ttg tcc tta tct ctc	834																	
Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu Ser Leu Ser Leu																		
230 235 240 245																		
tca tcg tct tta gag gct gca gca aaa gcg gaa gag tat aga aac att	882																	
Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Asn Ile																		
245 250 255 260																		

## MBI15 Sequence Listing.ST25

tac tac gga gcc aat tct tct aac gca tca cct cat cat caa tac aat Tyr Tyr Gly Ala Asn Ser Ser Asn Ala Ser Pro His His Gln Tyr Asn 265 270 275	930
caa ttc aag act ctt ctt gct aat tct tct caa cat cac cat caa gta Gln Phe Lys Thr Leu Leu Ala Asn Ser Ser Gln His His His Gln Val 280 285 290	978
tta aac caa ttc cga tca tct ccg gct gct tct tcc tct tcc atg gca Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser Ser Ser Met Ala 295 300 305	1026
gcg gtc aat atc tta aga aac tcg agg tac aca acg gcc gcg caa gag Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr Ala Ala Gln Glu 310 315 320	1074
ttg ttg gaa gag ttt tgt agt gtt gga aga gga ttt ttg aag aag aac Leu Leu Glu Glu Phe Cys Ser Val Gly Arg Gly Phe Leu Lys Lys Asn 325 330 335 340	1122
aaa ctt ggg aac agc tca aac cct aat act tgc ggt ggt gat ggt ggt Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly Gly Asp Gly Gly 345 350 355	1170
ggc agc tct cct tcg tcg gcc gga gca aac aag gag cat cct cct tta Gly Ser Ser Pro Ser Ser Ala Gly Ala Asn Lys Glu His Pro Pro Leu 360 365 370	1218
tcg gcg tct gat cgg att gag cat caa aga agg aaa gtg aaa cta ctc Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys Val Lys Leu Leu 375 380 385	1266
acc atg ctt gaa gag gtg gac cga cgg tac aac cat tac tgc gag caa Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln 390 395 400	1314
atg cag atg gtt gtg aac tct ttc gac ata gta atg ggc cac ggt gcg Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met Gly His Gly Ala 405 410 415 420	1362
gca tta ccg tac acc gca ttg gct caa aaa gct atg tca aga cat ttt Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met Ser Arg His Phe 425 430 435	1410
aga tgc ctt aaa gat gca gtt gcg gct cag ctt aag cag agt tgc gaa Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys Gln Ser Cys Glu 440 445 450	1458
ctt ctt ggg gac aaa gat gca gcg gga atc tct tct tcc ggg tta aca Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser Ser Gly Leu Thr 455 460 465	1506
aaa ggt gaa act ccg cgt ttg cgt ttg cta gag caa agt ttg cgt cag Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln 470 475 480	1554
caa cgt gcg ttt cat caa atg ggt atg atg gaa caa gaa gct tgg cgg Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln Glu Ala Trp Arg 485 490 495 500	1602
cca caa cgc ggt ttg cct gaa cgc tcc gtc aat ata ctt aga gct tgg Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile Leu Arg Ala Trp 505 510 515	1650
ctc ttc gaa cat ttc ctt cac ccg tat cca agt gat gca gat aaa cac Leu Phe Glu His Phe Leu His Pro Tyr Ser Pro Ser Asp Ala Asp Lys His 520 525 530	1698
cta ttg gct cga cag act ggt tta tcc aga aat cag gta tca aat tgg Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp 535 540 545	1746
ttc ata aat gct agg gtt cgt tta tgg aaa cca atg gtg gaa gaa atg Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met 550 555	1794

MBI15 Sequence Listing.ST25

550	555	560	
tac caa caa gaa tca	aaa gaa aga gaa aga gaa gag gaa tta gaa gag		1842
Tyr Gln Gln Glu Ser	Lys Glu Arg Glu Arg Glu Glu Glu Leu Glu Glu		
565	570	575	580
aac gaa gaa gat caa gaa aca aaa aac agc aac gac gac aag agc aca			1890
Asn Glu Glu Asp Gln Glu Thr Lys Asn Ser Asn Asp Asp Lys Ser Thr			
	585	590	595
aaa tcc aac aac aat gaa agc aac ttc act gcc gtt cgg acc act tca			1938
Lys Ser Asn Asn Asn Glu Ser Asn Phe Thr Ala Val Arg Thr Thr Ser			
	600	605	610
caa act cca acg aca acc gca cca gac gca tca gac gca gac gca gca			1986
Gln Thr Pro Thr Thr Thr Ala Pro Asp Ala Ser Asp Ala Asp Ala Ala			
	615	620	625
gta gcg aca ggc cac cgt cta aga tcc aac att aat gct tac gaa aac			2034
Val Ala Thr Gly His Arg Leu Arg Ser Asn Ile Asn Ala Tyr Glu Asn			
	630	635	640
gac gct tca tca ctt cta ctc cct tcc tct tat tcc aac gcc gcc gct			2082
Asp Ala Ser Ser Leu Leu Leu Pro Ser Ser Tyr Ser Asn Ala Ala Ala			
	645	650	655
cct gcc gct gtt tct gac gac ttg aat tct cgt tac ggt ggc tca gac			2130
Pro Ala Ala Val Ser Asp Asp Leu Asn Ser Arg Tyr Gly Gly Ser Asp			
	665	670	675
gcg ttt tcc gcc gtt gcc acg tgt caa caa agt gta ggt ggg ttc gat			2178
Ala Phe Ser Ala Val Ala Thr Cys Gln Gln Ser Val Gly Gly Phe Asp			
	680	685	690
gat gct gac atg gat ggt gtt aac gtt ata agg ttt ggg aca aac cct			2226
Asp Ala Asp Met Asp Gly Val Asn Val Ile Arg Phe Gly Thr Asn Pro			
	695	700	705
act ggt gac gtg tct ctc acg ctt ggt tta cgc cac gct gga aac atg			2274
Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His Ala Gly Asn Met			
	710	715	720
cct gac aaa gac gct tct ttc tgc gtt aga gag ttt ggg ggt ttt tag			2322
Pro Asp Lys Asp Ala Ser Phe Cys Val Arg Glu Phe Gly Gly Phe			
	725	730	735
tttgcttttg tcaactccatt taattaatta attatagttt tccattctta cttattttaa			2382
ttgaaaatct atttttgtct cttaaaagtc caaacaatac attagtctag ccctcctctg			2442
cttttttttt tctatctcgt gaagagaaga aaacgatacg taaatccctt cgaaaactaa			2502
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&lt;210&gt; 18

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 18

Met Gly Ile Thr Lys Thr Ser Pro Asn Thr Thr Ile Leu Leu Lys Thr  
1 5 10 15

Phe His Asn Asn Ser Met Ser Gln Asp Tyr His His His His His His  
20 25 30

Asn Gln His Gln Gly Gly Ile Phe Asn Phe Ser Asn Gly Phe Asp Arg  
35 40 45

Ser Asp Ser Pro Asn Leu Thr Thr Gln Gln Lys Gln Glu His Gln Arg

## 50

55

60

Tyr Glu Ser Ala Gly Met Leu Ser Glu Met Phe Asn Phe Pro Gly Ser  
85 90 95

Ser Gly Gly Gly Arg Asp Leu Asp Leu Gly Gln Ser Phe Arg Ser Asn  
100 105 110

Arg Gln Leu Leu Glu Glu Gln His Gln Asn Ile Pro Ala Met Asn Ala  
115 120 125

Thr Asp Ser Ala Thr Ala Thr Ala Ala Ala Met Gln Leu Phe Leu Met  
130 135 140

Asn Pro Pro Pro Pro Gln Gln Pro Pro Ser Pro Ser Ser Thr Thr Ser  
145 150 155 160

Pro Arg Ser His His Asn Ser Ser Thr Leu His Met Leu Leu Pro Ser  
165 170 175

Pro Ser Thr Asn Thr Thr His His Gln Asn Tyr Thr Asn His Met Ser  
180 185 190

Met His Gln Leu Pro His Gln His His Gln Gln Ile Ser Thr Trp Gln  
195 200 205

Ser Ser Pro Asp His His His His His His Asn Ser Gln Thr Glu Ile  
210 215 220

Gly Thr Val His Val Glu Asn Ser Gly Gly His Gly Gly Gln Gly Leu  
225 230 235 240

Ser Leu Ser Leu Ser Ser Ser Leu Glu Ala Ala Ala Lys Ala Glu Glu  
245 250 255

Tyr Arg Asn Ile Tyr Tyr Gly Ala Asn Ser Ser Asn Ala Ser Pro His  
260 265 270

His Gln Tyr Asn Gln Phe Lys Thr Leu Leu Ala Asn Ser Ser Gln His  
275 280 285

His His Gln Val Leu Asn Gln Phe Arg Ser Ser Pro Ala Ala Ser Ser  
290 295 300

Ser Ser Met Ala Ala Val Asn Ile Leu Arg Asn Ser Arg Tyr Thr Thr  
305 310 315 320

Ala Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser Val Gly Arg Gly Phe  
325 330 335

Leu Lys Lys Asn Lys Leu Gly Asn Ser Ser Asn Pro Asn Thr Cys Gly  
340 345 350

MBI15 Sequence Listing.ST25

Gly Asp Gly Gly Gly Ser Ser Pro Ser Ser Ala Gly Ala Asn Lys Glu  
 355 360 365

His Pro Pro Leu Ser Ala Ser Asp Arg Ile Glu His Gln Arg Arg Lys  
 370 375 380

Val Lys Leu Leu Thr Met Leu Glu Glu Val Asp Arg Arg Tyr Asn His  
 385 390 400

Tyr Cys Glu Gln Met Gln Met Val Val Asn Ser Phe Asp Ile Val Met  
 405 410 415

Gly His Gly Ala Ala Leu Pro Tyr Thr Ala Leu Ala Gln Lys Ala Met  
 420 425 430

Ser Arg His Phe Arg Cys Leu Lys Asp Ala Val Ala Ala Gln Leu Lys  
 435 440 445

Gln Ser Cys Glu Leu Leu Gly Asp Lys Asp Ala Ala Gly Ile Ser Ser  
 450 455 460

Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg Leu Arg Leu Leu Glu Gln  
 465 470 475 480

Ser Leu Arg Gln Gln Arg Ala Phe His Gln Met Gly Met Met Glu Gln  
 485 490 495

Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro Glu Arg Ser Val Asn Ile  
 500 505 510

Leu Arg Ala Trp Leu Phe Glu His Phe Leu His Pro Tyr Pro Ser Asp  
 515 520 525

Ala Asp Lys His Leu Leu Ala Arg Gln Thr Gly Leu Ser Arg Asn Gln  
 530 535 540

Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met  
 545 550 555 560

Val Glu Glu Met Tyr Gln Gln Glu Ser Lys Glu Arg Glu Arg Glu Glu  
 565 570 575

Glu Leu Glu Glu Asn Glu Glu Asp Gln Glu Thr Lys Asn Ser Asn Asp  
 580 585 590

Asp Lys Ser Thr Lys Ser Asn Asn Asn Glu Ser Asn Phe Thr Ala Val  
 595 600 605

Arg Thr Thr Ser Gln Thr Pro Thr Thr Thr Ala Pro Asp Ala Ser Asp  
 610 615 620

Ala Asp Ala Ala Val Ala Thr Gly His Arg Leu Arg Ser Asn Ile Asn  
 625 630 635 640

Ala Tyr Glu Asn Asp Ala Ser Ser Leu Leu Leu Pro Ser Ser Tyr Ser  
 645 650 655

## MBI15 Sequence Listing.ST25

Asn Ala Ala Ala Pro Ala Ala Val Ser Asp Asp Leu Asn Ser Arg Tyr  
660 665 670

Gly Gly Ser Asp Ala Phe Ser Ala Val Ala Thr Cys Gln Gln Ser Val  
675 680 685

Gly Gly Phe Asp Asp Ala Asp Met Asp Gly Val Asn Val Ile Arg Phe  
690 695 700

Gly Thr Asn Pro Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His  
705 710 715 720

Ala Gly Asn Met Pro Asp Lys Asp Ala Ser Phe Cys Val Arg Glu Phe  
725 730 735

Gly Gly Phe

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<212> DNA  
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<223> G591

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tcaaagtcctc tgtcttttagc tcaaacc atg gct agt aac aac cct cac gac aac 114  
Met Ala Ser Asn Asn Pro His Asp Asn  
1 5  
ctt tct gac caa act cct tct gat gat ttc ttc gag caa atc ctc ggc 162  
Leu Ser Asp Gln Thr Pro Ser Asp Asp Phe Phe Glu Gln Ile Leu Gly  
10 15 20 25  
ctt cct aac ttc tca gcc tct tct gcc gcc ggt tta tct gga gtt gac 210  
Leu Pro Asn Phe Ser Ala Ser Ser Ala Ala Gly Leu Ser Gly Val Asp  
30 35 40  
gga gga tta ggt ggt gga gca ccg cct atg atg ctg cag ttg ggt tcc 258  
Gly Gly Leu Gly Gly Gly Ala Pro Pro Met Met Leu Gln Leu Gly Ser  
45 50 55  
gga gaa gaa gga agt cac atg ggt ggc tta gga gga agt gga cca act 306  
Gly Glu Glu Gly Ser His Met Gly Gly Leu Gly Gly Ser Gly Pro Thr  
60 65 70  
ggg ttt cac aat cag atg ttt cct ttg ggg tta agt ctt gat caa ggg 354  
Gly Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly  
75 80 85  
aaa gga cct ggg ttt ctt aga cct gaa gga gga cat gga agt ggg aaa 402  
Lys Gly Pro Gly Phe Leu Arg Pro Glu Gly Gly His Gly Ser Gly Lys  
90 95 100 105  
aga ttc tca gat gat gtt gtt gat aat cga tgt tct tct atg aaa cct 450  
Arg Phe Ser Asp Asp Val Val Asp Asn Arg Cys Ser Ser Met Lys Pro  
110 115 120  
gtt ttc cac ggg cag cct atg caa cag cca cct cca tcg gcc cca cat 498  
Val Phe His Gly Gln Pro Met Gln Gln Pro Pro Pro Ser Ala Pro His  
125 130 135

MBI15 Sequence Listing.ST25

cag cct act tca atc cgt ccc agg gtt cga gct agg cgt ggt cag gct Gln Pro Thr Ser Ile Arg Pro Arg Val Arg Ala Arg Arg Gly Gln Ala 140 145 150	546
act gat cca cat agc atc gct gag cgg cta cgt aga gaa aga ata gca Thr Asp Pro His Ser Ile Ala Glu Arg Leu Arg Arg Glu Arg Ile Ala 155 160 165	594
gaa cgg atc agg gcg ctg cag gaa ctt gta cct act gtg aac aag acc Glu Arg Ile Arg Ala Met Ile Asp Glu Ile Val Asp Tyr Val Lys Phe Leu 170 175 180 185	642
gat aga gct gct atg atc gat gag att gtc gat tat gta aag ttt ctc Asp Arg Ala Ala Met Ile Asp Glu Ile Val Asp Tyr Val Lys Phe Leu 190 195 200	690
agg ctc caa gtc aag gtt ttg agc atg aac cga ctt ggt gga gcc ggt Arg Leu Gln Val Lys Val Leu Ser Met Asn Arg Leu Gly Gly Ala Gly 205 210 215	738
gcg gtt gct cca ctt gtt act gat atg cct ctt tca tca tca gtt gag Ala Val Ala Pro Leu Val Thr Asp Met Pro Leu Ser Ser Ser Val Glu 220 225 230	786
gat gaa acg ggt gag ggt gga agg act ccg caa cca gcg tgg gag aaa Asp Glu Thr Gly Glu Gly Thr Arg Thr Pro Gln Pro Ala Trp Glu Lys 235 240 245	834
tgg tct aac gat ggg act gaa cgt caa gtg gct aaa ctg atg gaa gag Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu 250 255 260 265	882
aac gtt gga gcc gcg atg cag ctt ctt caa tca aag gct ctt tgt atg Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Met 270 275 280	930
atg cca atc tca ttg gca atg gca att tac cat tct caa cct ccg gat Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp 285 290 295	978
aca tct tca gtg gtc aag cct gag aac aat cct cca cag tag Thr Ser Ser Val Val Lys Pro Glu Asn Asn Pro Pro Gln 300 305 310	1020
gatttctgca ataaagagtt tgtacagcta atccaactgt ccaacatggg tttttcttct 1080	
gctctaataga ctctgggttc ttctctcctc tctcaccgac ttgaaaggta aaaaagtga 1140	
aaaggctttg tagatggaat caatgtagga ttgtagtag agggcaaaaa aatgtcatat 1200	
agctcaattg atcaagtctt aaaaaaaaaa aaaaaaaaaa 1240	

&lt;210&gt; 20

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 20

Met Ala Ser Asn Asn Pro His Asp Asn Leu Ser Asp Gln Thr Pro Ser  
1 5 10 15

Asp Asp Phe Phe Glu Gln Ile Leu Gly Leu Pro Asn Phe Ser Ala Ser  
20 25 30

Ser Ala Ala Gly Leu Ser Gly Val Asp Gly Gly Leu Gly Gly Gly Ala  
35 40 45

Pro Pro Met Met Leu Gln Leu Gly Ser Gly Glu Glu Gly Ser His Met  
50 55 60

## MBI15 Sequence Listing.ST25

Gly Gly Leu Gly Gly Ser Gly Pro Thr Gly Phe His Asn Gln Met Phe  
 65 70 75 80  
 Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly Pro Gly Phe Leu Arg  
 85 90 95  
 Pro Glu Gly Gly His Gly Ser Gly Lys Arg Phe Ser Asp Asp Val Val  
 100 105 110  
 Asp Asn Arg Cys Ser Ser Met Lys Pro Val Phe His Gly Gln Pro Met  
 115 120 125  
 Gln Gln Pro Pro Pro Ser Ala Pro His Gln Pro Thr Ser Ile Arg Pro  
 130 135 140  
 Arg Val Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala  
 145 150 155 160  
 Glu Arg Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ala Leu Gln  
 165 170 175  
 Glu Leu Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp  
 180 185 190  
 Glu Ile Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu  
 195 200 205  
 Ser Met Asn Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr  
 210 215 220  
 Asp Met Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gly Glu Gly Gly  
 225 230 235 240  
 Arg Thr Pro Gln Pro Ala Trp Glu Lys Trp Ser Asn Asp Gly Thr Glu  
 245 250 255  
 Arg Gln Val Ala Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln  
 260 265 270  
 Leu Leu Gln Ser Lys Ala Leu Cys Met Met Pro Ile Ser Leu Ala Met  
 275 280 285  
 Ala Ile Tyr His Ser Gln Pro Pro Asp Thr Ser Ser Val Val Lys Pro  
 290 295 300  
 Glu Asn Asn Pro Pro Gln  
 305 310

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 <212> DNA  
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 <222> (109)..(966)  
 <223> G525

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Met Asp Tyr
1

gag gca tca aga atc gtc gaa atg gta gaa gat gaa gaa cat ata gat 165
Glu Ala Ser Arg Ile Val 10 Met Val Glu Asp 15 Glu Glu His Ile Asp

cta cca cca gga ttc aga ttt cac cct act gat gaa gaa ctc ata act 213
Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr 35
20 25 30 35

cac tac ctc aaa cca aag gtt ttc aac act ttc ttc tct gct act gcc 261
His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser Ala Thr Ala 50
40 45 50

att ggt gaa gtt gat ctc aac aag att gag cct tgg gac tta cca tgg 309
Ile Gly Glu Val Asp Leu Asn Lys 60 Ile Glu Pro Trp Asp 65 Leu Pro Trp
55 60 65

aag gct aag atg gga gaa aaa gaa tgg tat ttc ttc tgt gtg aga gac 357
Lys Ala Lys Met Gly Glu Lys 75 Trp Tyr Phe Phe Cys Val Arg Asp 80
70 75 80

cgg aaa tac ccg acc ggt tta agg aca aac cgg gcg aca gaa gcc ggt 405
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly 95
85 90 95

tat tgg aaa gcc aca gga aaa gac aaa gag ata ttc aag gga aaa tca 453
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Ser 115
100 105 110 115

ctt gtg ggt atg aag aaa act ttg gtt ttc tat aaa gga aga gct cct 501
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro 130
120 125 130

aaa gga gtt aaa acc aat tgg gtt atg cat gaa tat cgt tta gaa ggc 549
Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg 145 Leu Glu Gly 145
135 140 145

aaa tat tgt att gaa aat ctt ccc caa aca gct aag aac gaa tgg gtt 597
Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn Glu Trp Val 160
150 155 160

ata tgt cgt gtt ttc caa aaa cgt gcc gat ggt aca aag gtt cca atg 645
Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys Val Pro Met 175
165 170 175

tca atg ctt gat cca cac att aac cga atg gaa cca gcc ggt tta cct 693
Ser Met Leu Asp Pro His Ile Asn Arg Met 190 Glu Pro Ala Gly Leu Pro 195
180 185 190

tcg tta atg gat tgt tct caa cga gac tcc ttc acc ggt tcg tcg tct 741
Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly Ser Ser Ser 210
200 205 210

cac gtg acc tgc ttc tcc gac caa gaa acc gaa gac aaa aga ctt gtc 789
His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys Arg Leu Val 225
215 220 225

cac gag tcc aaa gac ggt ttt ggt tct ctg ttt tac tcg gat cct ctg 837
His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser Asp Pro Leu 240
230 235 240

ttt tta caa gac aat tat tcg cta atg aag ctg ttg ctt gac ggt caa 885
Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu Asp Gly Gln 255
245 250 255

gaa act caa ttc tcc ggc aaa cct ttc gac ggt cgt gat tcg tcc ggt 933
Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp Ser Ser Gly 275
260 265 270 275

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## MBI15 Sequence Listing.ST25

aca gaa gaa ttg gat tgc gtt tgg aat ttc tga gttgtataag ttatgttgta 986  
 Thr Glu Glu Leu Asp Cys Val Trp Asn Phe  
 280 285

gacttgtagt agtcattgtt tcgtgtgtgt gaatgaatat tcttggtaca tttttttgta 1046

aaaaaggaga aaaaaatatg ctgaaagtc aattgctttt gttatgtagc attagtgttt 1106

tttatgtact caatagactt cctaattaaa taaaaatctt aatttatttg ccaaaaaaaaa 1166

aaaaaaaaaaa aaa 1179

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<211> 285

<212> PRT

<213> Arabidopsis thaliana

<400> 22

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 20 25 30

Leu Ile Thr His Tyr Leu Lys Pro Lys Val Phe Asn Thr Phe Phe Ser  
 35 40 45

Ala Thr Ala Ile Gly Glu Val Asp Leu Asn Lys Ile Glu Pro Trp Asp  
 50 55 60

Leu Pro Trp Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys  
 65 70 75 80

Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr  
 85 90 95

Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys  
 100 105 110

Gly Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Lys Gly  
 115 120 125

Arg Ala Pro Lys Gly Val Lys Thr Asn Trp Val Met His Glu Tyr Arg  
 130 135 140

Leu Glu Gly Lys Tyr Cys Ile Glu Asn Leu Pro Gln Thr Ala Lys Asn  
 145 150 155 160

Glu Trp Val Ile Cys Arg Val Phe Gln Lys Arg Ala Asp Gly Thr Lys  
 165 170 175

Val Pro Met Ser Met Leu Asp Pro His Ile Asn Arg Met Glu Pro Ala  
 180 185 190

Gly Leu Pro Ser Leu Met Asp Cys Ser Gln Arg Asp Ser Phe Thr Gly  
 195 200 205

Ser Ser Ser His Val Thr Cys Phe Ser Asp Gln Glu Thr Glu Asp Lys  
 210 215 220

## MBI15 Sequence Listing.ST25

Arg Leu Val His Glu Ser Lys Asp Gly Phe Gly Ser Leu Phe Tyr Ser  
225 230 235 240

Asp Pro Leu Phe Leu Gln Asp Asn Tyr Ser Leu Met Lys Leu Leu Leu  
245 250 255

Asp Gly Gln Glu Thr Gln Phe Ser Gly Lys Pro Phe Asp Gly Arg Asp  
260 265 270

Ser Ser Gly Thr Glu Glu Leu Asp Cys Val Trp Asn Phe  
275 280 285

<210> 23  
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Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro  
5 10 15

ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag 153  
Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys  
20 25 30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc 201  
Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu  
35 40 45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac 249  
Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp  
50 55 60 65

aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag 297  
Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys  
70 75 80

tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt 345  
Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly  
85 90 95

cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga 393  
His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly  
100 105 110

gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act 441  
Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Ser Ala Val Thr  
115 120 125

act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt 489  
Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe  
130 135 140 145

cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga 537  
Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly  
150 155 160

aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg 585

MBI15 Sequence Listing.ST25

Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly	
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Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile	
180 185 190	
cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg	681
Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met	
195 200 205	
agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt	729
Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu	
210 215 220 225	
caa ctt taa ggaaatttac ttagacgata agatttcggtt tgtataactgt	778
Gln Leu	
tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa	838
ttcttcttgt tctttcattt taaaaattat taaaccgatt ctttaccaca aa	890
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Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr	
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Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn	
35 40 45	
Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg	
50 55 60	
Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr	
65 70 75 80	
Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly	
85 90 95	
Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly	
100 105 110	
Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val	
115 120 125	
Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser	
130 135 140	
Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu	
145 150 155 160	
Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala	
165 170 175	

## MBI15 Sequence Listing.ST25

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn  
 180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val  
 195 200 205

Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys  
 210 215 220

Leu Gln Leu  
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 cacacctatt attctcttgg tgtgtttgtg tgttacatat acgtgtgagt acatactttg 180  
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 Met Val Ser Ala Leu  
 1 5  
 agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt 344  
 Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro Val Lys Gln Glu Leu  
 10 15 20  
 gat aaa tcg gat caa cat caa cca gac caa gat caa cca aga aga aga 392  
 Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp Gln Pro Arg Arg Arg  
 25 30 35  
 cac tat aga ggc gta agg cag aga cca tgg ggt aaa tgg gcg gca gaa 440  
 His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu  
 40 45 50  
 atc cgc gat cca aag aaa gca gcc cgt gtc tgg ctc ggg act ttc gag 488  
 Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu  
 55 60 65  
 acg gca gag gaa gct gct tta gcc tat gac cga gct gcc ctc aaa ttc 536  
 Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe  
 70 75 80 85  
 aaa ggc acc aag gct aaa ctg aac ttc cct gaa cgg gtc caa ggc cct 584  
 Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro  
 90 95 100  
 act acc acc aca acc att tct cat gca cca aga gga gtt agt gaa tcc 632  
 Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser  
 105 110 115  
 atg aac tca cct cct cct cga cct ggt cca cct tca act act act act 680  
 Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro Ser Thr Thr Thr Thr  
 120 125 130  
 tcg tgg cca atg act tat aac cag gac ata ctt caa tac gct cag ttg 728  
 Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu Gln Tyr Ala Gln Leu  
 135 140 145

## MBI15 Sequence Listing.ST25

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 150 155 160 165

ttc agt caa cct ttt tca acg cct tct tca tct tct tct tcc tcc caa 824  
 Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser Ser Ser Ser Gln  
 170 175 180

cag acg cag caa cag cag cta caa caa caa caa cag cag cgt gaa gaa 872  
 Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Arg Glu Glu  
 185 190 195

gaa gag aag aat tat ggt tac aat tat tat aac tac cca aga gaa taa 920  
 Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn Tyr Pro Arg Glu  
 200 205 210

tctaattatt attggtggtc gaatcagttt tataaatagc tatcatagtt tcatttttgg 980

ttcccgtaac ctttggtgca tggaaaatat gaatgaacga gggacatgtg taacaatttg 1040

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aatcatttga cggtcacaaaa aaaaaa 1126

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Val Lys Gln Glu Leu Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp  
 20 25 30

Gln Pro Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly  
 35 40 45

Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp  
 50 55 60

Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg  
 65 70 75 80

Ala Ala Leu Lys Phe Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu  
 85 90 95

Arg Val Gln Gly Pro Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg  
 100 105 110

Gly Val Ser Glu Ser Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro  
 115 120 125

Ser Thr Thr Thr Thr Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu  
 130 135 140

Gln Tyr Ala Gln Leu Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr  
 145 150 155 160

Tyr Thr Ser Thr Leu Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser  
 165 170 175

## MBI15 Sequence Listing.ST25

Ser Ser Ser Ser Gln Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln  
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195 200 205

Tyr Pro Arg Glu  
210

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Met Asp Gly Ser Ser Phe Leu Asp Ile Ser Leu Asp  
1 5 10  
ctc aac acc aat cct ttc tcc gca aaa ctt ccg aag aag gag gtc tca 159  
Leu Asn Thr Asn Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser  
15 20 25  
gtt ttg gct tct act cac tta aag agg aaa tgg ttg gag caa gac gag 207  
Val Leu Ala Ser Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu  
30 35 40  
agc gca agt gag tta cga gag gag cta aac aga gtt aat tca gag aac 255  
Ser Ala Ser Glu Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn  
45 50 55 60  
aag aag cta aca gag atg tta gct aga gtc tgt gag agc tac aac gaa 303  
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu  
65 70 75  
cta cat aat cat ttg gag aag ctt cag agt cgc cag agc cct gaa atc 351  
Leu His Asn His Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile  
80 85 90  
gag cag acc gat ata ccg ata aag aaa aga aaa caa gac ccg gat gag 399  
Glu Gln Thr Asp Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu  
95 100 105  
ttc tta ggc ttt cct att gga ctc agt agt gga aaa act gag aac agc 447  
Phe Leu Gly Phe Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser  
110 115 120  
tcc agc aac gaa gat cat cat cat cat cat cag caa cat gag cag aaa 495  
Ser Ser Asn Glu Asp His His His His His Gln Gln His Glu Gln Lys  
125 130 135 140  
aat cag ctt ctt tca tgt aaa aga cca gtc act gat agc ttc aac aaa 543  
Asn Gln Leu Leu Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys  
145 150 155  
gca aaa gtt tcg act gtc tac gtg cct act gaa aca tcg gac aca agc 591  
Ala Lys Val Ser Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser  
160 165 170  
ttg aca gtt aaa gat gga ttt caa tgg agg aaa tac gga caa aag gtt 639  
Leu Thr Val Lys Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val  
175 180 185

## MBI15 Sequence Listing.ST25

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aca aga gac aac ccg tca cct aga gct tac ttt aga tgc tcg ttt gca    687
Thr Arg Asp Asn Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala
190                               195                               200

ccg tct tgt cca gta aaa aag aag gta caa cgc agc gca gag gat cca    735
Pro Ser Cys Pro Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro
205                               210                               215                               220

tct tta ctt gta gcg aca tac gaa ggg acg cat aac cac ttg ggt cca    783
Ser Leu Leu Val Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro
225                               230                               235

aat gct tct gaa ggg gat gct aca agc cag ggt ggg tca agc aca gtg    831
Asn Ala Ser Glu Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val
240                               245                               250

act ttg gat ctg gtt aat ggc tgt cat aga cta gcg ttg gag aaa aac    879
Thr Leu Asp Leu Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn
255                               260                               265

gaa agg gat aat acg atg caa gag gtt ctg att caa caa atg gcg tca    927
Glu Arg Asp Asn Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser
270                               275                               280

tcg tta aca aaa gat tcg aaa ttt aca gct gct ctt gct gct gct ata    975
Ser Leu Thr Lys Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile
285                               290                               295                               300

tct ggg agg tta atg gag caa tct aga aca tga acgttttttag tgaatgtatt 1028
Ser Gly Arg Leu Met Glu Gln Ser Arg Thr
305                               310

gtttttgttt gtttagaatg attcttcggtt ttcgaaattgt gtcttttcgat taggagataa 1088

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aaaa 1152

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<212> PRT
<213> Arabidopsis thaliana

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Pro Phe Ser Ala Lys Leu Pro Lys Lys Glu Val Ser Val Leu Ala Ser
20 25 30

Thr His Leu Lys Arg Lys Trp Leu Glu Gln Asp Glu Ser Ala Ser Glu
35 40 45

Leu Arg Glu Glu Leu Asn Arg Val Asn Ser Glu Asn Lys Lys Leu Thr
50 55 60

Glu Met Leu Ala Arg Val Cys Glu Ser Tyr Asn Glu Leu His Asn His
65 70 75 80

Leu Glu Lys Leu Gln Ser Arg Gln Ser Pro Glu Ile Glu Gln Thr Asp
85 90 95

Ile Pro Ile Lys Lys Arg Lys Gln Asp Pro Asp Glu Phe Leu Gly Phe
100 105 110

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MBI15 Sequence Listing.ST25

Pro Ile Gly Leu Ser Ser Gly Lys Thr Glu Asn Ser Ser Ser Asn Glu  
 115 120 125

Asp His His His His His Gln Gln His Glu Gln Lys Asn Gln Leu Leu  
 130 135 140

Ser Cys Lys Arg Pro Val Thr Asp Ser Phe Asn Lys Ala Lys Val Ser  
 145 150 155 160

Thr Val Tyr Val Pro Thr Glu Thr Ser Asp Thr Ser Leu Thr Val Lys  
 165 170 175

Asp Gly Phe Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp Asn  
 180 185 190

Pro Ser Pro Arg Ala Tyr Phe Arg Cys Ser Phe Ala Pro Ser Cys Pro  
 195 200 205

Val Lys Lys Lys Val Gln Arg Ser Ala Glu Asp Pro Ser Leu Leu Val  
 210 215 220

Ala Thr Tyr Glu Gly Thr His Asn His Leu Gly Pro Asn Ala Ser Glu  
 225 230 235 240

Gly Asp Ala Thr Ser Gln Gly Gly Ser Ser Thr Val Thr Leu Asp Leu  
 245 250 255

Val Asn Gly Cys His Arg Leu Ala Leu Glu Lys Asn Glu Arg Asp Asn  
 260 265 270

Thr Met Gln Glu Val Leu Ile Gln Gln Met Ala Ser Ser Leu Thr Lys  
 275 280 285

Asp Ser Lys Phe Thr Ala Ala Leu Ala Ala Ala Ile Ser Gly Arg Leu  
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Met Glu Gln Ser Arg Thr  
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cca cct ccc tca agc atc tac gct cct ccg atg ctg gtg aat tgc tcc 103  
 Pro Pro Pro Ser Ser Ile Tyr Ala Pro Pro Met Leu Val Asn Cys Ser  
 5 10 15

ggt tgc cgg acg cct ctc cag ctc cca tcc ggc gcc cga tct att cgc 151  
 Gly Cys Arg Thr Pro Leu Gln Leu Pro Ser Gly Ala Arg Ser Ile Arg  
 20 25 30 35

## MBI15 Sequence Listing.ST25

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cct cct ccg caa cct tcc tcc gcc cct tct ccg cct ccc caa atc cac Pro Pro Pro 55 Ser Ser Ala 60 Ser Pro Pro 65 Gln Ile His	247
gcg cct ccc ggt cag ctg cct cac ccc cat ggc agg aag agg gcc gtg Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys Arg Ala Val 70 75 80	295
atc tgt ggc atc tcg tat cgt ttc tct cgc cac gag ctc aaa ggc tgc Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu Lys Gly Cys 85 90 95	343
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ttc tcc cca gat tca att ctc atg ctt acc gag gaa gaa act gat cca Phe Ser Pro Asp Ser 120 Ile Leu Met Leu Thr 125 Glu Glu Glu Thr 130 Asp Pro	439
tat cgt atc ccg acc aag caa aac atg agg atg gca ttg tat tgg ctc Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu Tyr Trp Leu 135 140 145	487
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cat ggt tcg cgt caa aga aac tac aac ggt gat gaa gtt gat ggc tat His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val Asp Gly Tyr 165 170 175	583
gat gaa aca ctc tgt cct ctg gat ttt gaa act cag ggg atg att gta Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly Met Ile Val 180 185 190 195	631
gac gat gag atc aac gca acc att gta cgc cct ctt cca cat ggt gtc Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro His Gly Val 200 205 210	679
aag ctc cat tca att atc gat gct tgc cat agt ggt acc gtt ctg gat Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr Val Leu Asp 215 220 225	727
tta ccc ttc cta tgc aga atg aac aga gct ggg cag tat gtg tgg gag Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr Val Trp Glu 230 235 240	775
gat cat cgg cct agg tca ggt ttg tgg aaa gga act gct ggt gga gaa Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala Gly Gly Glu 245 250 255	823
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att caa gca att gaa cgc agc gca caa ggc aca acc tat gga agc ctt Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr Gly Ser Leu 295 300 305	967
ctg aat tct atg cgc acc aca ata agg aat aca ggg aat gat ggt ggt Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn Asp Gly Gly 310 315 320	1015
ggg agt ggt gga gtt gtg acg act gtg ctg agc atg ctt ctg aca ggg Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu Leu Thr Gly	1063

MBI15 Sequence Listing.ST25

325	330	335	
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340	345	350	355
caa aca ttc gat gtc tat gca aag cct ttc act ctc tag taaaggacaa			1160
Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu			
	360	365	
gtcacttttt atgtatagcg agtgtgattt gagaatccgt ccatataacc accttttgtt			1220
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Ser Ile Arg Cys Ala Leu Cys Gln Ala Val Thr His Ile Ala Asp Pro			
	35	40	45
Arg Thr Ala Pro Pro Pro Gln Pro Ser Ser Ala Pro Ser Pro Pro Pro			
	50	55	60
Gln Ile His Ala Pro Pro Gly Gln Leu Pro His Pro His Gly Arg Lys			
65	70	75	80
Arg Ala Val Ile Cys Gly Ile Ser Tyr Arg Phe Ser Arg His Glu Leu			
	85	90	95
Lys Gly Cys Ile Asn Asp Ala Lys Cys Met Arg His Leu Leu Ile Asn			
	100	105	110
Lys Phe Lys Phe Ser Pro Asp Ser Ile Leu Met Leu Thr Glu Glu Glu			
	115	120	125
Thr Asp Pro Tyr Arg Ile Pro Thr Lys Gln Asn Met Arg Met Ala Leu			
	130	135	140
Tyr Trp Leu Val Gln Gly Cys Thr Ala Gly Asp Ser Leu Val Phe His			
145	150	155	160
Tyr Ser Gly His Gly Ser Arg Gln Arg Asn Tyr Asn Gly Asp Glu Val			
	165	170	175
Asp Gly Tyr Asp Glu Thr Leu Cys Pro Leu Asp Phe Glu Thr Gln Gly			
	180	185	190
Met Ile Val Asp Asp Glu Ile Asn Ala Thr Ile Val Arg Pro Leu Pro			
	195	200	205
His Gly Val Lys Leu His Ser Ile Ile Asp Ala Cys His Ser Gly Thr			

## MBI15 Sequence Listing.ST25

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210
215
220
Val Leu Asp Leu Pro Phe Leu Cys Arg Met Asn Arg Ala Gly Gln Tyr
225                230                235                240

Val Trp Glu Asp His Arg Pro Arg Ser Gly Leu Trp Lys Gly Thr Ala
                245                250                255

Gly Gly Glu Ala Ile Ser Ile Ser Gly Cys Asp Asp Asp Gln Thr Ser
                260                265                270

Ala Asp Thr Ser Ala Leu Ser Lys Ile Thr Ser Thr Gly Ala Met Thr
                275                280                285

Phe Cys Phe Ile Gln Ala Ile Glu Arg Ser Ala Gln Gly Thr Thr Tyr
                290                295                300

Gly Ser Leu Leu Asn Ser Met Arg Thr Thr Ile Arg Asn Thr Gly Asn
305                310                315                320

Asp Gly Gly Gly Ser Gly Gly Val Val Thr Thr Val Leu Ser Met Leu
                325                330                335

Leu Thr Gly Gly Ser Ala Ile Gly Gly Leu Arg Gln Glu Pro Gln Leu
                340                345                350

Thr Ala Cys Gln Thr Phe Asp Val Tyr Ala Lys Pro Phe Thr Leu
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<223> G378

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cct ctt tcg tca agt cct tct ctt ggg aat ttc gtc gaa cgc att aaa      96
Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys
                20                25                30

gac gct tgt cat ttc ctt gtc tct gct gtt ttg ggt acc att atc tcc     144
Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser
                35                40                45

gcg atc ttg acc ttc ttc ttc gca cta gtg ggc aca ttg cta ggg gca     192
Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala
                50                55                60

ctt aca gga gct ttg ata ggt caa gaa act gag agt ggt ttc att aga     240
Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg
65                70                75                80

gga gca gca att gga gcc att tcg gga gct gtt ttc tct atc gag gtc     288
Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val
                85                90                95

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MBI15 Sequence Listing.ST25

ttt gaa tca tct ctg gat ctc tgg aaa tcc gat gag tcg ggt ttc gga Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly 100 105 110	336
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ctt gta cga gag cgc att ggt cct gca atg cta agt gca gtg caa agt Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser 130 135 140	432
caa atg gga gct gtg gat aca gct ttt gat gat cac aca agc ctt ttt Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe 145 150 155 160	480
gat aca gga ggc tca aaa gga ttg aca gga gac ctt gtt gag aaa atc Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile 165 170 175	528
cca aag atg aca atc act ggc aac aat aac act gat gct tct gag aac Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn 180 185 190	576
aca gac tca tgt tct gtt tgt ctt cag gat ttc cag ctc ggt gaa aca Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr 195 200 205	624
gtt aga agc ttg cct cat tgt cat cac atg ttt cac tta cct tgc ata Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile 210 215 220	672
gac aat tgg ctc ctt aga cac ggt tct tgc ccg atg tgt aga cgt gat Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp 225 230 235 240	720
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 <212> PRT  
 <213> Arabidopsis thaliana

<400> 32

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Pro Leu Ser Ser Ser Pro Ser Leu Gly Asn Phe Val Glu Arg Ile Lys 20 25 30
Asp Ala Cys His Phe Leu Val Ser Ala Val Leu Gly Thr Ile Ile Ser 35 40 45
Ala Ile Leu Thr Phe Phe Phe Ala Leu Val Gly Thr Leu Leu Gly Ala 50 55 60
Leu Thr Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg 65 70 75 80
Gly Ala Ala Ile Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val 85 90 95
Phe Glu Ser Ser Leu Asp Leu Trp Lys Ser Asp Glu Ser Gly Phe Gly 100 105 110

## MBI15 Sequence Listing.ST25

Cys Phe Leu Tyr Leu Ile Asp Val Ile Val Ser Leu Leu Ser Gly Arg  
115 120 125

Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser  
130 135 140

Gln Met Gly Ala Val Asp Thr Ala Phe Asp Asp His Thr Ser Leu Phe  
145 150 155 160

Asp Thr Gly Gly Ser Lys Gly Leu Thr Gly Asp Leu Val Glu Lys Ile  
165 170 175

Pro Lys Met Thr Ile Thr Gly Asn Asn Asn Thr Asp Ala Ser Glu Asn  
180 185 190

Thr Asp Ser Cys Ser Val Cys Leu Gln Asp Phe Gln Leu Gly Glu Thr  
195 200 205

Val Arg Ser Leu Pro His Cys His His Met Phe His Leu Pro Cys Ile  
210 215 220

Asp Asn Trp Leu Leu Arg His Gly Ser Cys Pro Met Cys Arg Arg Asp  
225 230 235 240

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<212> DNA  
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<223> G569

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cggcaagttt gtatctagaa aggatcgatt ggtgagggtca atagtgggtg gtgggtttta 180  
gta atg gaa gac ggt gag ctt gat ttc tcc aat cag gaa gtg ttt tcg 228  
Met Glu Asp Gly Glu Leu Asp Phe Ser Asn Gln Glu Val Phe Ser 15  
agt tcg gag atg ggt gaa tta cca cct agc aat tgt tcg atg gat agt 276  
Ser Ser Glu Met Gly Glu Leu Pro Pro Ser Asn Cys Ser Met Asp Ser 20 25 30  
ttc ttt gat ggg ctt tta atg gat act aat gct gct tgt acc cac act 324  
Phe Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr 35 40 45  
cac acc tgt aac ccc act gga cca gag aac act cat act cac acg tgc 372  
His Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys 50 55 60  
ttc cat gtc cac acc aag att ctc ccg gat gag agc gat gaa aaa gtt 420  
Phe His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val 65 70 75

## MBI15 Sequence Listing.ST25

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tct act gat gat aca gct gag tct tgt ggg aag aag ggt gaa aag aga    468
Ser Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg
80                      85                      90                      95

cct ttg gga aac cgg gaa gcg gtt aga aag tat aga gag aag aag aag    516
Pro Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys
100                    105                    110

gct aaa gct gct tct ttg gag gat gag gtt gca agg ctt agg gcg gtg    564
Ala Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val
115                    120                    125

aat cag cag ctg gtg aag agg ttg caa aat cag gct acc ttg gaa gct    612
Asn Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala
130                    135                    140

gag gtt tcg agg ctt aag tgt ttg ctt gtg gat ttg aga gga aga ata    660
Glu Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile
145                    150                    155

gat gga gag att gga tct ttt cct tat cag aaa cct atg gct gca aat    708
Asp Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn
160                    165                    170                    175

att cct tct ttc tcg cac atg atg aat cct tgt aat gta caa tgt gat    756
Ile Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp
180                    185                    190

gat gaa gtt tat tgc cct cag aat gtg ttt gga gtg aat agc caa gaa    804
Asp Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu
195                    200                    205

ggg gcc tcg atc aat gac caa ggg tta agt ggt tgt gat ttt gat cag    852
Gly Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln
210                    215                    220

cta caa tgc atg gct aat cag aac tta aat gga aat gga aac gga tca    900
Leu Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser
225                    230                    235

ttc agc aac gtc aat aca tct gtc tcg aat aag aga aaa ggt ggg cat    948
Phe Ser Asn Val Asn Thr Ser Val Ser Asn Lys Arg Lys Gly Gly His
240                    245                    250                    255

cgt gca tca aga gca gtt tga agcatcatca agcttgact atctatttcc    999
Arg Ala Ser Arg Ala Val
260

accagcatag atattgtatt ccaaataagt tgtagagttc agctgcagga tcagcttcgc    1059

tcagctttga ggggttggtg gtgtggtctt tctttgtggc acgagtgaga tctatggaca    1119

gaaccagat ttagtagtag tagaggcagg atttcgactt ccactaacca tcatgttgct    1179

tggtgaagaa caaggtatgc ccatgaagca cactgttttg tacattgagc ttgaggggct    1239

gtctctgac tagccttact gtaacattgc aacgttctca caattgtgat cccaagttgc    1299

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aaaaaaaaaa a                                                    1370

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<213> Arabidopsis thaliana

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## MBI15 Sequence Listing.ST25

20

25

30

Phe Asp Gly Leu Leu Met Asp Thr Asn Ala Ala Cys Thr His Thr His  
35 40 45

Thr Cys Asn Pro Thr Gly Pro Glu Asn Thr His Thr His Thr Cys Phe  
50 55 60

His Val His Thr Lys Ile Leu Pro Asp Glu Ser Asp Glu Lys Val Ser  
65 70 75 80

Thr Asp Asp Thr Ala Glu Ser Cys Gly Lys Lys Gly Glu Lys Arg Pro  
85 90 95

Leu Gly Asn Arg Glu Ala Val Arg Lys Tyr Arg Glu Lys Lys Lys Ala  
100 105 110

Lys Ala Ala Ser Leu Glu Asp Glu Val Ala Arg Leu Arg Ala Val Asn  
115 120 125

Gln Gln Leu Val Lys Arg Leu Gln Asn Gln Ala Thr Leu Glu Ala Glu  
130 135 140

Val Ser Arg Leu Lys Cys Leu Leu Val Asp Leu Arg Gly Arg Ile Asp  
145 150 155 160

Gly Glu Ile Gly Ser Phe Pro Tyr Gln Lys Pro Met Ala Ala Asn Ile  
165 170 175

Pro Ser Phe Ser His Met Met Asn Pro Cys Asn Val Gln Cys Asp Asp  
180 185 190

Glu Val Tyr Cys Pro Gln Asn Val Phe Gly Val Asn Ser Gln Glu Gly  
195 200 205

Ala Ser Ile Asn Asp Gln Gly Leu Ser Gly Cys Asp Phe Asp Gln Leu  
210 215 220

Gln Cys Met Ala Asn Gln Asn Leu Asn Gly Asn Gly Asn Gly Ser Phe  
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Ala Ser Arg Ala Val  
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<223> G558

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MBI15 Sequence Listing.ST25

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acatttggtc ctgattcatt tcctattggt tcgtattgtc tgtgcacaca agagaaattt	180
caagaagttg ttactaaaag agaggccaca agtggatatt gtctttgtta tcaagtgtta	240
gtacagaaaa gtgggtgagaa agtaat atg gct gat acc agt ccg aga act gat	293
Met Ala Asp Thr Ser Pro Arg Thr Asp	
1 5	
gtc tca aca gat gac gac aca gat cat cct gat ctt ggg tcg gag gga	341
Val Ser Thr Asp Asp Asp Thr Asp His Pro Asp Leu Gly Ser Glu Gly	
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gca cta gtg aat act gct gct tct gat tcg agt gac cga tcg aag gga	389
Ala Leu Val Asn Thr Ala Ala Ser Asp Ser Ser Asp Arg Ser Lys Gly	
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aag atg gat caa aag act ctt cgt agg ctt gct caa aac cgt gag gca	437
Lys Met Asp Gln Lys Thr Leu Arg Arg Leu Ala Gln Asn Arg Glu Ala	
45 50 55	
gca agg aaa agc aga ttg agg aag aag gct tat gtt cag cag cta gag	485
Ala Arg Lys Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu	
60 65 70	
aac agc cgc ttg aaa cta acc cag ctt gag cag gag ctg caa aga gca	533
Asn Ser Arg Leu Lys Leu Thr Gln Leu Glu Gln Glu Leu Gln Arg Ala	
75 80 85	
aga cag cag ggc gtc ttc att tca ggc aca gga gac cag gcc cat tct	581
Arg Gln Gln Gly Val Phe Ile Ser Gly Thr Gly Asp Gln Ala His Ser	
90 95 100 105	
act ggt gga aat ggt gct ttg gcg ttt gat gct gaa cat tca cgg tgg	629
Thr Gly Gly Asn Gly Ala Leu Ala Phe Asp Ala Glu His Ser Arg Trp	
110 115 120	
ttg gaa gaa aag aac aag caa atg aac gag ctg agg tct gct ctg aat	677
Leu Glu Glu Lys Asn Lys Gln Met Asn Glu Leu Arg Ser Ala Leu Asn	
125 130 135	
gcg cat gca ggt gat tct gag ctt cga ata ata gtc gat ggt gtg atg	725
Ala His Ala Gly Asp Ser Glu Leu Arg Ile Ile Val Asp Gly Val Met	
140 145 150	
gct cac tat gag gag ctt ttc agg ata aag agc aat gca gct aag aat	773
Ala His Tyr Glu Glu Leu Phe Arg Ile Lys Ser Asn Ala Ala Lys Asn	
155 160 165	
gat gtc ttt cac ttg cta tct ggc atg tgg aaa aca cca gct gag aga	821
Asp Val Phe His Leu Leu Ser Gly Met Trp Lys Thr Pro Ala Glu Arg	
170 175 180 185	
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Cys Phe Leu Trp Leu Gly Gly Phe Arg Ser Ser Glu Leu Leu Lys Leu	
190 195 200	
ctg gcg aat cag ttg gag cca atg aca gag aga cag ttg atg ggc ata	917
Leu Ala Asn Gln Leu Glu Pro Met Thr Glu Arg Gln Leu Met Gly Ile	
205 210 215	
aat aac ctg caa cag aca tcg cag cag gct gaa gat gct ttg tct caa	965
Asn Asn Leu Gln Gln Thr Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln	
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Gly Met Glu Ser Leu Gln Gln Ser Leu Ala Asp Thr Leu Ser Ser Gly	
235 240 245	
act ctt ggt tca agt tca tca ggg aat gtc gca agc tac atg ggt cag	1061
Thr Leu Gly Ser Ser Ser Ser Gly Asn Val Ala Ser Tyr Met Gly Gln	
250 255 260 265	

## MBI15 Sequence Listing.ST25

atg gcc atg gca atg gga aag tta ggt aca ctc gaa gga ttt atc cgc 1109  
Met Ala Met Ala Met Gly Lys Leu Gly Thr Leu Glu Gly Phe Ile Arg  
270 275 280

cag gct gat aat ttg aga cta caa aca ttg caa cag atg ata aga gta 1157  
Gln Ala Asp Asn Leu Arg Leu Gln Thr Leu Gln Gln Met Ile Arg Val  
285 290 295

tta aca acg aga cag tca gca cgt gct cta ctt gca ata cac gat tac 1205  
Leu Thr Thr Arg Gln Ser Ala Arg Ala Leu Leu Ala Ile His Asp Tyr  
300 305 310

ttc tca cgg cta cga gct cta agc tcc tta tgg ctt gct cga ccc aga 1253  
Phe Ser Arg Leu Arg Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg  
315 320 325

gag tga aactgtatatt tggtcacatg tcagctgtac aaaatccata tggacacaaa 1309  
Glu  
330

accaggagag actattaatc aacacttgtc agattcttct taccaaattcc atcaacaaat 1369

aagcaaattt ctgggaaaca aaagactctt tgtatgtagg tttcttctac atggttgtgg 1429

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gttgtttata tagcatcttc gattatctta gaaaggttat tgaattttgt ttttttttgt 1549

tacttttgtg tgtggtaaag gtgttttaac cttgcaactt ctgtactgta atcatttaac 1609

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<400> 36

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Ser Asp Ser Ser Asp Arg Ser Lys Gly Lys Met Asp Gln Lys Thr Leu  
35 40 45

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg  
50 55 60

Lys Lys Ala Tyr Val Gln Gln Leu Glu Asn Ser Arg Leu Lys Leu Thr  
65 70 75 80

Gln Leu Glu Gln Glu Leu Gln Arg Ala Arg Gln Gln Gly Val Phe Ile  
85 90 95

Ser Gly Thr Gly Asp Gln Ala His Ser Thr Gly Gly Asn Gly Ala Leu  
100 105 110

Ala Phe Asp Ala Glu His Ser Arg Trp Leu Glu Glu Lys Asn Lys Gln  
115 120 125

Met Asn Glu Leu Arg Ser Ala Leu Asn Ala His Ala Gly Asp Ser Glu  
130 135 140

## MBI15 Sequence Listing.ST25

Leu Arg Ile Ile Val Asp Gly Val Met Ala His Tyr Glu Glu Leu Phe  
145 150 155 160

Arg Ile Lys Ser Asn Ala Ala Lys Asn Asp Val Phe His Leu Leu Ser  
165 170 175

Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu Trp Leu Gly Gly  
180 185 190

Phe Arg Ser Ser Glu Leu Leu Lys Leu Leu Ala Asn Gln Leu Glu Pro  
195 200 205

Met Thr Glu Arg Gln Leu Met Gly Ile Asn Asn Leu Gln Gln Thr Ser  
210 215 220

Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Glu Ser Leu Gln Gln  
225 230 235 240

Ser Leu Ala Asp Thr Leu Ser Ser Gly Thr Leu Gly Ser Ser Ser Ser  
245 250 255

Gly Asn Val Ala Ser Tyr Met Gly Gln Met Ala Met Ala Met Gly Lys  
260 265 270

Leu Gly Thr Leu Glu Gly Phe Ile Arg Gln Ala Asp Asn Leu Arg Leu  
275 280 285

Gln Thr Leu Gln Gln Met Ile Arg Val Leu Thr Thr Arg Gln Ser Ala  
290 295 300

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Met Asp Gly Glu Asp Phe Ala Gly Lys Ala  
1 5 10

gct gct gaa gcc aag gga ttg aac ccg gga tta atc gtg ctg ctt gtt 160  
Ala Ala Glu Ala Lys Gly Leu Asn Pro Gly Leu Ile Val Leu Val  
15 20 25

gtt gga ggt ccg ctt ctt gtg ttc cta atc gcc aac tac gtg ctt tac 208  
Val Gly Gly Pro Leu Leu Val Phe Leu Ile Ala Asn Tyr Val Leu Tyr  
30 35 40

## MBI15 Sequence Listing.ST25

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 Val Tyr Ala Gln Lys Asn Leu Pro Pro Arg Lys Lys Lys Pro Val Ser  
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aaa aag aag ctc aag cgg gag aag cta aag caa gga gtc cct gtc cct 304  
 Lys Lys Lys Leu Lys Arg Glu Lys Leu Lys Gln Gly Val Pro Val Pro  
           60                  65                  70

gga gaa taa aagccagctt aagcttcctt cacttggtgcc tccttcaaag 353  
 Gly Glu  
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cggtttttgt tcggttacca aatttcaccc ttgcgggttt ttttcttcct ttacttctgt 413

catgaggatt atctttgagg cct 436

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 <212> PRT  
 <213> Arabidopsis thaliana

<400> 38

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                   20                  25                  30

Val Phe Leu Ile Ala Asn Tyr Val Leu Tyr Val Tyr Ala Gln Lys Asn  
           35                  40                  45

Leu Pro Pro Arg Lys Lys Lys Pro Val Ser Lys Lys Lys Leu Lys Arg  
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Glu Lys Leu Lys Gln Gly Val Pro Val Pro Gly Glu  
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 aaatcaaaga gacttttgaa gattgtttcc caatttgcgt caatcgggat cgagtcaaat 180  
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 gtttggtttt aaacgtcttg gattcgaagt ggtaaggt atg gat gaa aat aat 294  
   Met Asp Glu Asn Asn  
   1                  5

gga ggt tca agc tca ctt cca cct ttc ctt act aaa aca tat gaa atg 342  
 Gly Gly Ser Ser Ser Leu Pro Pro Phe Leu Thr Lys Thr Tyr Glu Met  
                   10                  15                  20

ggt gat gat tct tct tct gac tcg gtc gtt gct tgg agc gaa aac aac 390  
 Val Asp Asp Ser Ser Ser Asp Ser Val Val Ala Trp Ser Glu Asn Asn

MBI15 Sequence Listing.ST25																
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40						45						50				
ccg Pro	aga Arg	ttc Phe	ttc Phe	aag Lys	cat His	aag Lys	aat Asn	ttc Phe	tca Ser	agt Ser	ttc Phe	atc Ile	cgt Arg	cag Gln	ctt Leu	486
55						60						65				
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70						75						80				
aat Asn	gat Asp	gat Asp	ttt Phe	gtt Val	aga Arg	ggt Gly	cga Arg	cct Pro	tac Tyr	ctt Leu	atg Met	aag Lys	aac Asn	att Ile	cat His	582
90						95						100				
aga Arg	cga Arg	aaa Lys	ccg Pro	gtt Val	cat His	agc Ser	cac His	tcg Ser	tta Leu	gtg Val	aat Asn	cta Leu	caa Gln	gcg Ala	caa Gln	630
105						110						115				
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120						125						130				
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135						140						145				
gag Glu	caa Gln	gaa Glu	cgg Arg	aaa Lys	gag Glu	ttt Phe	gag Glu	ctg Leu	caa Gln	gta Val	acg Thr	aca Thr	ttg Leu	aaa Lys	gat Asp	774
150						155						160				
cgg Arg	tta Leu	caa Gln	cat His	atg Met	gaa Glu	caa Gln	cat His	cag Gln	aaa Lys	tca Ser	ata Ile	gtg Val	gca Ala	tat Tyr	gtt Val	822
170						175						180				
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185						190						195				
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200						205						210				
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215						220						225				
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230						235						240				
agc Ser	atg Met	gat Asp	cat His	gat Asp	gca Ala	gct Ala	gag Glu	tca Ser	agt Ser	cta Leu	agt Ser	att Ile	ggc Gly	gat Asp	aca Thr	1062
250						255						260				
cga Arg	ccc Pro	aaa Lys	tca Ser	tcg Ser	aag Lys	att Ile	gat Asp	atg Met	aac Asn	tca Ser	gag Glu	ccg Pro	ccc Pro	gtt Val	acc Thr	1110
265						270						275				
gtt Val	act Thr	gcg Ala	cct Pro	gct Ala	cca Pro	aaa Lys	aca Thr	ggc Gly	gtt Val	aac Asn	gat Asp	gac Asp	ttt Phe	tgg Trp	gaa Glu	1158
280						285						290				
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295						300						305				
tca Ser	gag Glu	aga Arg	aga Arg	gat Asp	gtc Val	ggg Gly	aat Asn	gat Asp	aat Asn	aat Asn	ggg Gly	aat Asn	aag Lys	att Ile	gga Gly	1254
310						315						320				
aat Asn	caa Gln	agg Arg	acg Thr	tat Asp	tgg Val	tgg Val	aat Asn	tca Ser	ggg Gly	aat Asn	gta Val	aat Asn	aac Lys	att Ile	aca Thr	1302
325						330						335				

## MBI15 Sequence Listing.ST25

Asn Gln Arg Thr Tyr Trp Trp Asn Ser Gly Asn Val Asn Asn Ile Thr  
 330 335 340  
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 Glu Lys Ala Ser  
 345  
 actgagatta ttgtatgtgt tcattattta ttactctggt tctgtaaaaa caaatctctc 1417  
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 20 25 30  
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 35 40 45  
 Ser Arg Asp Leu Leu Pro Arg Phe Phe Lys His Lys Asn Phe Ser Ser  
 50 55 60  
 Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Val Asp Pro Glu  
 65 70 75 80  
 Lys Trp Glu Phe Leu Asn Asp Asp Phe Val Arg Gly Arg Pro Tyr Leu  
 85 90 95  
 Met Lys Asn Ile His Arg Arg Lys Pro Val His Ser His Ser Leu Val  
 100 105 110  
 Asn Leu Gln Ala Gln Asn Pro Leu Thr Glu Ser Glu Arg Arg Ser Met  
 115 120 125  
 Glu Asp Gln Ile Glu Arg Leu Lys Asn Glu Lys Glu Gly Leu Leu Ala  
 130 135 140  
 Glu Leu Gln Asn Gln Glu Gln Glu Arg Lys Glu Phe Glu Leu Gln Val  
 145 150 155 160  
 Thr Thr Leu Lys Asp Arg Leu Gln His Met Glu Gln His Gln Lys Ser  
 165 170 175  
 Ile Val Ala Tyr Val Ser Gln Val Leu Gly Lys Pro Gly Leu Ser Leu  
 180 185 190  
 Asn Leu Glu Asn His Glu Arg Arg Lys Arg Arg Phe Gln Glu Asn Ser  
 195 200 205  
 Leu Pro Pro Ser Ser Ser His Ile Glu Gln Val Glu Lys Leu Glu Ser  
 210 215 220

## MBI15 Sequence Listing.ST25

Ser Leu Thr Phe Trp Glu Asn Leu Val Ser Glu Ser Cys Glu Lys Ser  
225 230 235 240

Gly Leu Gln Ser Ser Ser Met Asp His Asp Ala Ala Glu Ser Ser Leu  
245 250 255

Ser Ile Gly Asp Thr Arg Pro Lys Ser Ser Lys Ile Asp Met Asn Ser  
260 265 270

Glu Pro Pro Val Thr Val Thr Ala Pro Ala Pro Lys Thr Gly Val Asn  
275 280 285

Asp Asp Phe Trp Glu Gln Cys Leu Thr Glu Asn Pro Gly Ser Thr Glu  
290 295 300

Gln Gln Glu Val Gln Ser Glu Arg Arg Asp Val Gly Asn Asp Asn Asn  
305 310 315 320

Gly Asn Lys Ile Gly Asn Gln Arg Thr Tyr Trp Trp Asn Ser Gly Asn  
325 330 335

Val Asn Asn Ile Thr Glu Lys Ala Ser  
340 345

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<223> G1006

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Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser Ile Thr  
5 10 15  
cgt cac ttg cta gga gga gga gga gag aac gag ctg cga ctc aat gag 153  
Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu Asn Glu  
20 25 30  
tca aca ccg agt tcg tgt ttc aca gag agt tgg gga ggt ttg cca ttg 201  
Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu Pro Leu  
35 40 45 50  
aaa gag aat gat tca gag gac atg ttg gtg tac gga ctc ctc aaa gat 249  
Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu Lys Asp  
55 60 65  
gcc ttc cat ttt gac acg tca tca tcg gac ttg agc tgt ctt ttt gat 297  
Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu Phe Asp  
70 75 80  
ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg atg gag 345  
Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala Met Glu  
85 90 95  
gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg aag gcg 393  
Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val Lys Ala  
100 105 110

## MBI15 Sequence Listing.ST25

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aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc gcg gcg      441
Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala
115                      120                      125                      130

gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta ggg acg      489
Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr
135                      140                      145

ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct gct ttt      537
Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala Ala Phe
150                      155                      160

agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg gtt aat      585
Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val Asn
165                      170                      175

tcc ggt gaa cct gac ccg gtt cgg atc acg tct aag aga tct tct tcg      633
Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser Ser Ser
180                      185                      190

tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac ggg aag      681
Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn Gly Lys
195                      200                      205                      210

ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg gtg cag      729
Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val Val Gln
215                      220                      225

gtg aag tgt gag gtt ggt gat gag aca cgt gtt gat gag tta ttg gtt      777
Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu Leu Val
230                      235                      240

tca taa gtttgatctt gtgtgttttg tagttgaata gttttgctat aaatggtgag      833
Ser

gcaccaagta aaagtgttcc cgtgatgtaa attagttact aaacagagcc atatatcttc      893
aatcaaaaaa aaaaaaaaaa                                          913

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<213> Arabidopsis thaliana

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Ile Thr Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu
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Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
35                      40                      45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
50                      55                      60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu
65                      70                      75                      80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
85                      90                      95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val
100                      105                      110

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## MBI15 Sequence Listing.ST25

Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe  
 115 120 125

Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu  
 130 135 140

Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala  
 145 150 155 160

Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg  
 165 170 175

Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser  
 180 185 190

Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn  
 195 200 205

Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val  
 210 215 220

Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu  
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Leu Val Ser

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 Lys Ser Gly Glu Arg Pro Lys Gln Arg Gln Arg Lys Gly Leu Trp Ser  
 5 10 15

cct gaa gaa gac cag aag ctc aag agt ttc atc ctc tct cgt ggc cat 154  
 Pro Glu Glu Asp Gln Lys Leu Lys Ser Phe Ile Leu Ser Arg Gly His  
 20 25 30

gct tgc tgg acc act gtt ccc atc cta gct gga ttg caa agg aat ggg 202  
 Ala Cys Trp Thr Thr Val Pro Ile Leu Ala Gly Leu Gln Arg Asn Gly  
 35 40 45 50

aaa agc tgc aga tta agg tgg att aat tac cta aga cca gga cta aag 250  
 Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys  
 55 60 65

agg ggg tcg ttt agt gaa gaa gaa gaa gag acc atc ttg act tta cat 298  
 Arg Gly Ser Phe Ser Glu Glu Glu Glu Glu Thr Ile Leu Thr Leu His  
 70 75 80

tct tcc ttg ggt aac aag tgg tct cgg att gca aaa tat tta ccg gga 346

MBI15 Sequence Listing.ST25

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		85					90					95					
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Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	His	Ser	Tyr	Leu	Lys	Lys		
	100					105					110						
aga	tgg	ctc	aaa	tct	caa	cca	caa	ctc	aaa	agc	caa	ata	tca	gac	ctc		442
Arg	Trp	Leu	Lys	Ser	Gln	Pro	Gln	Leu	Lys	Ser	Gln	Ile	Ser	Asp	Leu		
	115				120					125					130		
aca	gaa	tct	cct	tct	tca	cta	ctt	tct	tgc	ggg	aaa	aga	aat	ctg	gaa		490
Thr	Glu	Ser	Pro	Ser	Ser	Leu	Leu	Ser	Cys	Gly	Lys	Arg	Asn	Leu	Glu		
				135					140					145			
acc	gaa	acc	cta	gat	cac	gtg	atc	tcc	ttc	cag	aaa	ttt	tca	gag	aat		538
Thr	Glu	Thr	Leu	Asp	His	Val	Ile	Ser	Phe	Gln	Lys	Phe	Ser	Glu	Asn		
			150					155					160				
cca	act	tca	tca	cca	tcc	aaa	gaa	agc	aac	aac	aac	atg	atc	atg	aac		586
Pro	Thr	Ser	Ser	Pro	Ser	Lys	Glu	Ser	Asn	Asn	Asn	Met	Ile	Met	Asn		
		165				170						175					
aac	agt	aat	aac	ttg	cct	aaa	ctg	ttc	ttc	tct	gag	tgg	atc	agt	tct		634
Asn	Ser	Asn	Asn	Leu	Pro	Lys	Leu	Phe	Phe	Ser	Glu	Trp	Ile	Ser	Ser		
	180					185					190						
tca	aat	cca	cac	atc	gat	tac	tcc	tct	gct	ttt	aca	gat	tcc	aag	cac		682
Ser	Asn	Pro	His	Ile	Asp	Tyr	Ser	Ser	Ala	Phe	Thr	Asp	Ser	Lys	His		
	195			200					205					210			
att	aat	gaa	act	caa	gat	caa	atc	aat	gaa	gag	gaa	gtg	atg	atg	atc		730
Ile	Asn	Glu	Thr	Gln	Asp	Gln	Ile	Asn	Glu	Glu	Glu	Val	Met	Met	Ile		
				215					220				225				
aat	aac	aac	aac	tac	tct	tca	ctt	gag	gat	gtc	atg	ctc	cgt	aca	gat		778
Asn	Asn	Asn	Asn	Tyr	Ser	Ser	Leu	Glu	Asp	Val	Met	Leu	Arg	Thr	Asp		
			230				235					240					
ttt	ttg	cag	cct	gat	cat	gaa	tat	gca	aat	tat	tat	tct	tct	gga	gat		826
Phe	Leu	Gln	Pro	Asp	His	Glu	Tyr	Ala	Asn	Tyr	Tyr	Ser	Ser	Gly	Asp		
		245				250						255					
ttc	ttc	atc	aac	agt	gac	caa	aat	tat	gtc	taa	gaagagt	gaa	tatgatcgta				879
Phe	Phe	Ile	Asn	Ser	Asp	Gln	Asn	Tyr	Val								
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Trp	Ser	Pro	Glu	Glu	Asp	Gln	Lys	Leu	Lys	Ser	Phe	Ile	Leu	Ser	Arg		
		20						25					30				
Gly	His	Ala	Cys	Trp	Thr	Thr	Val	Pro	Ile	Leu	Ala	Gly	Leu	Gln	Arg		
		35					40					45					
Asn	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Ile	Asn	Tyr	Leu	Arg	Pro	Gly		
	50					55					60						
Leu	Lys	Arg	Gly	Ser	Phe	Ser	Glu	Glu	Glu	Glu	Glu	Thr	Ile	Leu	Thr		
65					70					75				80			

## MBI15 Sequence Listing.ST25

Leu His Ser Ser Leu Gly Asn Lys Trp Ser Arg Ile Ala Lys Tyr Leu  
                             85                            90                            95  
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser Tyr Leu  
                             100                            105                            110  
 Lys Lys Arg Trp Leu Lys Ser Gln Pro Gln Leu Lys Ser Gln Ile Ser  
                             115                            120                            125  
 Asp Leu Thr Glu Ser Pro Ser Ser Leu Leu Ser Cys Gly Lys Arg Asn  
                             130                            135                            140  
 Leu Glu Thr Glu Thr Leu Asp His Val Ile Ser Phe Gln Lys Phe Ser  
                             145                            150                            155                            160  
 Glu Asn Pro Thr Ser Ser Pro Ser Lys Glu Ser Asn Asn Asn Met Ile  
                             165                            170                            175  
 Met Asn Asn Ser Asn Asn Leu Pro Lys Leu Phe Phe Ser Glu Trp Ile  
                             180                            185                            190  
 Ser Ser Ser Asn Pro His Ile Asp Tyr Ser Ser Ala Phe Thr Asp Ser  
                             195                            200                            205  
 Lys His Ile Asn Glu Thr Gln Asp Gln Ile Asn Glu Glu Glu Val Met  
                             210                            215                            220  
 Met Ile Asn Asn Asn Asn Tyr Ser Ser Leu Glu Asp Val Met Leu Arg  
                             225                            230                            235                            240  
 Thr Asp Phe Leu Gln Pro Asp His Glu Tyr Ala Asn Tyr Tyr Ser Ser  
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 Gly Asp Phe Phe Ile Asn Ser Asp Gln Asn Tyr Val  
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 gaa tcc att tac ctc aac gaa caa caa caa caa caa caa gct tct 96  
 Glu Ser Ile Tyr Leu Asn Glu Gln Gln Gln Gln Gln Gln Ala Ser  
                             20                            25                            30  
 tct tcc tct gct gca tct ttc tcc gag att gtt tcc ggt gat gtt cga 144  
 Ser Ser Ser Ala Ala Ser Phe Ser Glu Ile Val Ser Gly Asp Val Arg  
                             35                            40                            45  
 aac aac gag atg gta ttt atc cca cca aca agc gac gta gcc gtc aac 192

MBI15 Sequence Listing.ST25																
Asn	Asn	Glu	Met	Val	Phe	Ile	Pro	Pro	Thr	Ser	Asp	Val	Ala	Val	Asn	
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gga	aac	gta	acg	gtg	tca	agt	aac	gat	cta	agc	ttt	cac	ggg	gga	gga	240
Gly	Asn	Val	Thr	Val	Ser	Ser	Asn	Asp	Leu	Ser	Phe	His	Gly	Gly	Gly	
65				70					75					80		
ctt	tct	tta	agt	ctt	ggg	aat	cag	atc	cag	tca	gct	gtc	tct	gtt	tct	288
Leu	Ser	Leu	Ser	Leu	Gly	Asn	Gln	Ile	Gln	Ser	Ala	Val	Ser	Val	Ser	
				85					90					95		
ccg	ttt	cag	tat	cat	tac	cag	aat	ctt	tcg	aac	caa	ttg	agt	tac	aat	336
Pro	Phe	Gln	Tyr	His	Tyr	Gln	Asn	Leu	Ser	Asn	Gln	Leu	Ser	Tyr	Asn	
			100					105					110			
aat	ctt	aat	cct	tct	act	atg	tct	gat	gag	aat	ggg	aag	agc	ttg	agt	384
Asn	Leu	Asn	Pro	Ser	Thr	Met		Asp	Glu	Asn	Gly	Lys	Ser	Leu	Ser	
		115					120					125				
gtt	cat	cag	cat	cac	tct	gat	caa	att	tta	cct	tcc	tct	gtt	tac	aac	432
Val	His	Gln	His	His	Ser	Asp	Gln	Ile	Leu	Pro	Ser	Ser	Val	Tyr	Asn	
						135					140					
aac	aat	ggg	aat	aat	ggg	gtt	gga	ttc	tac	aac	aat	tac	cgt	tac	gag	480
Asn	Asn	Gly	Asn	Asn	Gly	Val	Gly	Phe	Tyr	Asn	Asn	Tyr	Arg	Tyr	Glu	
145					150				155					160		
aca	tca	ggg	ttt	gtg	agt	agt	gta	ctg	aga	tct	cgt	tac	ctt	aaa	cca	528
Thr	Ser	Gly	Phe	Val	Ser	Ser	Val	Leu	Arg	Ser	Arg	Tyr	Leu	Lys	Pro	
				165					170					175		
aca	caa	caa	ttg	ctt	gat	gaa	gtt	gtt	agt	gta	agg	aaa	gat	ttg	aaa	576
Thr	Gln	Gln	Leu	Leu	Asp	Glu	Val	Val	Ser	Val	Arg	Lys	Asp	Leu	Lys	
				180				185					190			
ttg	ggg	aat	aag	aag	atg	aag	aat	gat	aaa	ggg	caa	gac	ttt	cac	aat	624
Leu	Gly	Asn	Lys	Lys	Met	Lys	Asn	Asp	Lys	Gly	Gln	Asp	Phe	His	Asn	
		195					200					205				
ggg	tct	agt	gat	aac	att	aca	gaa	gat	gat	aaa	tct	caa	tcg	cag	gag	672
Gly	Ser	Ser	Asp	Asn	Ile	Thr	Glu	Asp	Asp	Lys	Ser	Gln	Ser	Gln	Glu	
		210				215					220					
ttg	tct	cct	tca	gaa	cgt	cag	gag	cta	cag	agc	aag	aag	agc	aag	ctt	720
Leu	Ser	Pro	Ser	Glu	Arg	Gln	Glu	Leu	Gln	Ser	Lys	Lys	Ser	Lys	Leu	
					230					235					240	
tta	aca	atg	gtg	gat	gag	gta	gat	aaa	agg	tat	aac	caa	tac	cat	cat	768
Leu	Thr	Met	Val	Asp	Glu	Val	Asp	Lys	Arg	Tyr	Asn	Gln	Tyr	His	His	
				245					250					255		
caa	atg	gaa	gct	tta	gca	tcg	tct	ttc	gag	atg	gta	aca	ggg	ctt	gga	816
Gln	Met	Glu	Ala	Leu	Ala	Ser	Ser	Phe	Glu	Met	Val	Thr	Gly	Leu	Gly	
			260					265					270			
gca	gct	aag	cct	tac	aca	tcc	gta	gct	ctg	aat	aga	atc	tct	cgc	cat	864
Ala	Ala	Lys	Pro	Tyr	Thr	Ser	Val	Ala	Leu	Asn	Arg	Ile	Ser	Arg	His	
		275					280					285				
ttc	cgc	tgt	tta	cgc	gac	gcg	ata	aaa	gaa	cag	att	cag	gtg	atc	aga	912
Phe	Arg	Cys	Leu	Arg	Asp	Ala	Ile	Lys	Glu	Gln	Ile	Gln	Val	Ile	Arg	
		290				295					300					
ggg	aag	ctt	ggg	gag	aga	gag	act	tct	gat	gaa	caa	gga	gag	agg	ata	960
Gly	Lys	Leu	Gly	Glu	Arg	Glu	Thr	Ser	Asp	Glu	Gln	Gly	Glu	Arg	Ile	
				310					315					320		
ccg	cgt	ctt	agg	tac	tta	gat	caa	cgg	ttg	aga	caa	cag	aga	gct	ttg	1008
Pro	Arg	Leu	Arg	Tyr	Leu	Asp	Gln	Arg	Leu	Arg	Gln	Gln	Arg	Ala	Leu	
				325					330					335		
cat	caa	caa	ctt	gga	atg	gtt	aga	cca	gct	tgg	aga	cca	caa	aga	ggc	1056
His	Gln	Gln	Leu	Gly	Met	Val	Arg	Pro	Ala	Trp	Arg	Pro	Gln	Arg	Gly	
			340					345					350			

MBI15 Sequence Listing.ST25

tta cct gaa aac tct gtc tct Leu Pro Glu Asn Ser Val Ser	ata ctt cga gct tgg ctc ttt gag cat Ile Leu Arg Ala Trp Leu Phe Glu His	1104
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ttc ctt cat cca tat cct aaa gaa tca gag aaa atc atg ctt tca aag Phe Leu His Pro Tyr Pro Lys Glu Ser Glu Lys Ile Met Leu Ser Lys		1152
370	375	380
cag aca gga cta tgc aaa aac cag gtt gca aat tgg ttt att aac gcg Gln Thr Gly Leu Ser Lys Asn Gln Val Ala Asn Trp Phe Ile Asn Ala		1200
385	390	400
aga gtt cga cta tgg aaa cca atg att gaa gag atg tat aaa gaa gag Arg Val Arg Leu Trp Lys Pro Met Ile Glu Glu Met Tyr Lys Glu Glu		1248
405	410	415
ttt gga gaa tca gca gag tta ctc tct aac tct aat caa gac acc aaa Phe Gly Glu Ser Ala Glu Leu Leu Ser Asn Ser Asn Gln Asp Thr Lys		1296
420	425	430
aaa atg cag gaa aca tct cag ctc aaa cac gaa gac tct tcg tct tcg Lys Met Gln Glu Thr Ser Gln Leu Lys His Glu Asp Ser Ser Ser Ser		1344
435	440	445
caa caa cag aat cag gga aac aac aac aac aac atc cca tat aca tct Gln Gln Gln Asn Gln Gly Asn Asn Asn Asn Ile Pro Tyr Thr Ser		1392
450	455	460
gat gca gaa caa aac cta gtc ttt gca gat cct aaa cca gac cgt gct Asp Ala Glu Gln Asn Leu Val Phe Ala Asp Pro Lys Pro Asp Arg Ala		1440
465	470	480
act act gga gat tac gac agc ttg atg aac tat cat ggg ttt ggt att Thr Thr Gly Asp Tyr Asp Ser Leu Met Asn Tyr His Gly Phe Gly Ile		1488
485	490	495
gat gat tac aat cgt tac gtt ggc ctt gga aac caa caa gat ggc aga Asp Asp Tyr Asn Arg Tyr Val Gly Leu Gly Asn Gln Gln Asp Gly Arg		1536
500	505	510
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515	520	
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Ser Ser Ser Ala Ala Ser Phe Ser Glu Ile Val Ser Gly Asp Val Arg 35 40 45		
Asn Asn Glu Met Val Phe Ile Pro Pro Thr Ser Asp Val Ala Val Asn 50 55 60		
Gly Asn Val Thr Val Ser Ser Asn Asp Leu Ser Phe His Gly Gly Gly 65 70 75 80		
Leu Ser Leu Ser Leu Gly Asn Gln Ile Gln Ser Ala Val Ser Val Ser 85 90 95		

## MBI15 Sequence Listing.ST25

Pro Phe Gln Tyr His Tyr Gln Asn Leu Ser Asn Gln Leu Ser Tyr Asn  
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 Asn Leu Asn Pro Ser Thr Met Ser Asp Glu Asn Gly Lys Ser Leu Ser  
 115 120 125  
 Val His Gln His His Ser Asp Gln Ile Leu Pro Ser Ser Val Tyr Asn  
 130 135 140  
 Asn Asn Gly Asn Asn Gly Val Gly Phe Tyr Asn Asn Tyr Arg Tyr Glu  
 145 150 155 160  
 Thr Ser Gly Phe Val Ser Ser Val Leu Arg Ser Arg Tyr Leu Lys Pro  
 165 170 175  
 Thr Gln Gln Leu Leu Asp Glu Val Val Ser Val Arg Lys Asp Leu Lys  
 180 185 190  
 Leu Gly Asn Lys Lys Met Lys Asn Asp Lys Gly Gln Asp Phe His Asn  
 195 200 205  
 Gly Ser Ser Asp Asn Ile Thr Glu Asp Asp Lys Ser Gln Ser Gln Glu  
 210 215 220  
 Leu Ser Pro Ser Glu Arg Gln Glu Leu Gln Ser Lys Lys Ser Lys Leu  
 225 230 235 240  
 Leu Thr Met Val Asp Glu Val Asp Lys Arg Tyr Asn Gln Tyr His His  
 245 250 255  
 Gln Met Glu Ala Leu Ala Ser Ser Phe Glu Met Val Thr Gly Leu Gly  
 260 265 270  
 Ala Ala Lys Pro Tyr Thr Ser Val Ala Leu Asn Arg Ile Ser Arg His  
 275 280 285  
 Phe Arg Cys Leu Arg Asp Ala Ile Lys Glu Gln Ile Gln Val Ile Arg  
 290 295 300  
 Gly Lys Leu Gly Glu Arg Glu Thr Ser Asp Glu Gln Gly Glu Arg Ile  
 305 310 315 320  
 Pro Arg Leu Arg Tyr Leu Asp Gln Arg Leu Arg Gln Gln Arg Ala Leu  
 325 330 335  
 His Gln Gln Leu Gly Met Val Arg Pro Ala Trp Arg Pro Gln Arg Gly  
 340 345 350  
 Leu Pro Glu Asn Ser Val Ser Ile Leu Arg Ala Trp Leu Phe Glu His  
 355 360 365  
 Phe Leu His Pro Tyr Pro Lys Glu Ser Glu Lys Ile Met Leu Ser Lys  
 370 375 380  
 Gln Thr Gly Leu Ser Lys Asn Gln Val Ala Asn Trp Phe Ile Asn Ala  
 385 390 395 400

## MBI15 Sequence Listing.ST25

Arg Val Arg Leu Trp Lys Pro Met Ile Glu Glu Met Tyr Lys Glu Glu  
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Phe Gly Glu Ser Ala Glu Leu Leu Ser Asn Ser Asn Gln Asp Thr Lys  
420 425 430

Lys Met Gln Glu Thr Ser Gln Leu Lys His Glu Asp Ser Ser Ser Ser  
435 440 445

Gln Gln Gln Asn Gln Gly Asn Asn Asn Asn Asn Ile Pro Tyr Thr Ser  
450 455 460

Asp Ala Glu Gln Asn Leu Val Phe Ala Asp Pro Lys Pro Asp Arg Ala  
465 470 475 480

Thr Thr Gly Asp Tyr Asp Ser Leu Met Asn Tyr His Gly Phe Gly Ile  
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Asp Asp Tyr Asn Arg Tyr Val Gly Leu Gly Asn Gln Gln Asp Gly Arg  
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Tyr Ser Asn Pro His Gln Leu His Asp Phe Val Val  
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<223> G965

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Met Gly Leu Ala Thr Thr Thr Ser Ser Met Ser Gln Asp  
1 5 10  
tat cat cat cac caa gga atc ttt tcc ttc tct aat gga ttc cac cga 159  
Tyr His His His Gln Gly Ile Phe Ser Phe Ser Asn Gly Phe His Arg  
15 20 25  
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Ser Ser Ser Thr Thr His Gln Glu Glu Val Asp Glu Ser Ala Val Val  
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Ser Gly Ala Gln Ile Pro Val Tyr Glu Thr Ala Gly Met Leu Ser Glu  
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atg ttt gct tac cct ggc gga ggt ggc ggc ggt tcc ggt gga gag att 303  
Met Phe Ala Tyr Pro Gly Gly Gly Gly Gly Gly Ser Gly Gly Glu Ile  
65 70 75  
ctt gat cag tct act aaa cag ttg cta gag caa caa aac cgt cac aac 351  
Leu Asp Gln Ser Thr Lys Gln Leu Leu Glu Gln Gln Asn Arg His Asn  
80 85 90  
aac aac aat aac tca act ctt cat atg tta tta cca aat cat cat caa 399  
Asn Asn Asn Asn Ser Thr Leu His Met Leu Leu Pro Asn His His Gln  
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## MBI15 Sequence Listing.ST25

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Gly Phe Ala Phe Thr Asp Glu Asn Thr Met Gln Pro Gln Gln Gln	
110 115 120 125	
cac ttt aca tgg cca tct tcc tcc tcc gat cat cat caa aac cga gat	495
His Phe Thr Trp Pro Ser Ser Ser Ser Asp His His Gln Asn Arg Asp	
130 135 140	
atg atc gga acc gtc cac gtg gaa gga gga aag ggt ttg tct tta tct	543
Met Ile Gly Thr Val His Val Glu Gly Gly Lys Gly Leu Ser Leu Ser	
145 150 155	
ctc tca tct tca tta gcc gca gct aaa gcc gag gaa tat aga agc att	591
Leu Ser Ser Ser Leu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Ser Ile	
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tat tgt gca gcc gtt gat gga act tct tct tct tct aac gca tcc gct	639
Tyr Cys Ala Ala Val Asp Gly Thr Ser Ser Ser Ser Asn Ala Ser Ala	
175 180 185	
cat cat cat caa ttc aat cag ttc aag aat ctt ctt ctt gag aat tct	687
His His His Gln Phe Asn Gln Phe Lys Asn Leu Leu Leu Glu Asn Ser	
190 195 200 205	
tct tct caa cat cat cac cat caa gtt gtt gga cat ttt ggt tca tca	735
Ser Ser Gln His His His His Gln Val Val Gly His Phe Gly Ser Ser	
210 215 220	
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Ser Ser Ser Pro Met Ala Ala Ser Ser Ser Ile Gly Gly Ile Tyr Thr	
225 230 235	
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Leu Arg Asn Ser Lys Tyr Thr Lys Pro Ala Gln Glu Leu Leu Glu Glu	
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Phe Cys Ser Val Gly Arg Gly His Phe Lys Lys Asn Lys Leu Ser Arg	
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Asn Asn Ser Asn Pro Asn Thr Thr Gly Gly Gly Gly Gly Gly Gly Ser	
270 275 280 285	
tcg tca tcg gcc gga aca gct aat gat agt cct cct ttg tct ccg gct	975
Ser Ser Ser Ala Gly Thr Ala Asn Asp Ser Pro Pro Leu Ser Pro Ala	
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gat cgg att gaa cat caa aga aga aaa gtc aag cta cta tct atg ctt	1023
Asp Arg Ile Glu His Gln Arg Arg Lys Val Lys Leu Leu Ser Met Leu	
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gaa gag gtg gac cga cgg tac aac cac tac tgc gaa caa atg caa atg	1071
Glu Glu Val Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln Met Gln Met	
320 325 330	
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Val Val Asn Ser Phe Asp Gln Val Met Gly Tyr Gly Ala Ala Val Pro	
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Tyr Thr Thr Leu Ala Gln Lys Ala Met Ser Arg His Phe Arg Cys Leu	
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Lys Asp Ala Val Ala Val Gln Leu Lys Arg Ser Cys Glu Leu Leu Gly	
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gat aaa gag gcg gca ggg gct gca tcc tcg ggg tta acc aaa ggg gaa	1263
Asp Lys Glu Ala Ala Gly Ala Ala Ser Ser Gly Leu Thr Lys Gly Glu	
385 390 395	
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Thr Pro Arg Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln Gln Arg Ala	

MBI15 Sequence Listing.ST25

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ttt cat cat atg ggt atg atg gag caa gag gca tgg aga ccg caa cgt Phe His His Met Gly Met Met Glu Gln Glu Ala Trp Arg Pro Gln Arg 415 420 425			1359
ggg ttg cct gaa cgc tcc gtt aat atc ctt aga gct tgg cta ttc gag Gly Leu Pro Glu Arg Ser Val Asn Ile Leu Arg Ala Trp Leu Phe Glu 430 435 440 445			1407
cat ttt ctt aat ccg tac cca agc gat gct gat aag cac ctc tta gca His Phe Leu Asn Pro Tyr Pro Ser Asp Ala Asp Lys His Leu Leu Ala 450 455 460			1455
cga cag act ggt tta tcc aga aat cag gtg tca aat tgg ttc ata aat Arg Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile Asn 465 470 475			1503
gct agg gtt cgc cta tgg aaa cca atg gtg gaa gag atg tat caa caa Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr Gln Gln 480 485 490			1551
gaa gca aaa gaa aga gaa gaa gca gaa gaa gaa aat gaa aat caa caa Glu Ala Lys Glu Arg Glu Glu Ala Glu Glu Glu Asn Glu Asn Gln Gln 495 500 505			1599
caa caa aga aga cag caa caa aca aac aac aac gac acg aaa ccc aac Gln Gln Arg Arg Gln Gln Gln Thr Asn Asn Asn Asp Thr Lys Pro Asn 510 515 520 525			1647
aac aat gaa aac aac ttc act gtc ata acc gca caa act cca acg acg Asn Asn Glu Asn Asn Phe Thr Val Ile Thr Ala Gln Thr Pro Thr Thr 530 535 540			1695
atg aca tcg aca cat cac gaa aac gac tct tca ttc ctc tct tcc gtc Met Thr Ser Thr His His Glu Asn Asp Ser Ser Phe Leu Ser Ser Val 545 550 555			1743
gcc gcc gct tct cac gcc ggt tca gac gcg ttc acc gtc gcc acg tgt Ala Ala Ala Ser His Gly Gly Ser Asp Ala Phe Thr Val Ala Thr Cys 560 565 570			1791
cag caa gac gtc agt gac ttc cac gtc gac gga gat ggt gtg aac gtc Gln Gln Asp Val Ser Asp Phe His Val Asp Gly Asp Gly Val Asn Val 575 580 585			1839
ata aga ttc ggg acc aaa cag act ggt gac gtg tct ctt acg ctt ggt Ile Arg Phe Gly Thr Lys Gln Thr Gly Asp Val Ser Leu Thr Leu Gly 590 595 600 605			1887
cta cgc cac tct gcc aat att cct gat aag aac act tct ttc tcc gtt Leu Arg His Ser Gly Asn Ile Pro Asp Lys Asn Thr Ser Phe Ser Val 610 615 620			1935
aga gac ttt gga gat ttt tag tcttctttgt ttctcaattt attcatc Arg Asp Phe Gly Asp Phe 625			1983

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Thr Thr His Gln Glu Glu Val Asp Glu Ser Ala Val Val Ser Gly Ala

MBI15 Sequence Listing.ST25

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Tyr Pro Gly Gly Gly Gly Gly Gly Ser Gly Gly Glu Ile Leu Asp Gln		
65	70	75
Ser Thr Lys Gln Leu Leu Glu Gln Gln Asn Arg His Asn Asn Asn Asn		
85	90	95
Asn Ser Thr Leu His Met Leu Leu Pro Asn His His Gln Gly Phe Ala		
100	105	110
Phe Thr Asp Glu Asn Thr Met Gln Pro Gln Gln Gln Gln His Phe Thr		
115	120	125
Trp Pro Ser Ser Ser Ser Asp His His Gln Asn Arg Asp Met Ile Gly		
130	135	140
Thr Val His Val Glu Gly Gly Lys Gly Leu Ser Leu Ser Leu Ser Ser		
145	150	155
Ser Leu Ala Ala Ala Lys Ala Glu Glu Tyr Arg Ser Ile Tyr Cys Ala		
165	170	175
Ala Val Asp Gly Thr Ser Ser Ser Ser Asn Ala Ser Ala His His His		
180	185	190
Gln Phe Asn Gln Phe Lys Asn Leu Leu Leu Glu Asn Ser Ser Ser Gln		
195	200	205
His His His His Gln Val Val Gly His Phe Gly Ser Ser Ser Ser Ser		
210	215	220
Pro Met Ala Ala Ser Ser Ser Ile Gly Gly Ile Tyr Thr Leu Arg Asn		
225	230	235
Ser Lys Tyr Thr Lys Pro Ala Gln Glu Leu Leu Glu Glu Phe Cys Ser		
245	250	255
Val Gly Arg Gly His Phe Lys Lys Asn Lys Leu Ser Arg Asn Asn Ser		
260	265	270
Asn Pro Asn Thr Thr Gly Gly Gly Gly Gly Gly Ser Ser Ser Ser		
275	280	285
Ala Gly Thr Ala Asn Asp Ser Pro Pro Leu Ser Pro Ala Asp Arg Ile		
290	295	300
Glu His Gln Arg Arg Lys Val Lys Leu Leu Ser Met Leu Glu Glu Val		
305	310	315
Asp Arg Arg Tyr Asn His Tyr Cys Glu Gln Met Gln Met Val Val Asn		
325	330	335

MBI15 Sequence Listing.ST25

Ser Phe Asp Gln Val Met Gly Tyr Gly Ala Ala Val Pro Tyr Thr Thr  
340 345 350

Leu Ala Gln Lys Ala Met Ser Arg His Phe Arg Cys Leu Lys Asp Ala  
355 360 365

Val Ala Val Gln Leu Lys Arg Ser Cys Glu Leu Leu Gly Asp Lys Glu  
370 375 380

Ala Ala Gly Ala Ala Ser Ser Gly Leu Thr Lys Gly Glu Thr Pro Arg  
385 390 395 400

Leu Arg Leu Leu Glu Gln Ser Leu Arg Gln Gln Arg Ala Phe His His  
405 410 415

Met Gly Met Met Glu Gln Glu Ala Trp Arg Pro Gln Arg Gly Leu Pro  
420 425 430

Glu Arg Ser Val Asn Ile Leu Arg Ala Trp Leu Phe Glu His Phe Leu  
435 440 445

Asn Pro Tyr Pro Ser Asp Ala Asp Lys His Leu Leu Ala Arg Gln Thr  
450 455 460

Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val  
465 470 475 480

Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr Gln Gln Glu Ala Lys  
485 490 495

Glu Arg Glu Glu Ala Glu Glu Glu Asn Glu Asn Gln Gln Gln Gln Arg  
500 505 510

Arg Gln Gln Gln Thr Asn Asn Asn Asp Thr Lys Pro Asn Asn Asn Glu  
515 520 525

Asn Asn Phe Thr Val Ile Thr Ala Gln Thr Pro Thr Thr Met Thr Ser  
530 535 540

Thr His His Glu Asn Asp Ser Ser Phe Leu Ser Ser Val Ala Ala Ala  
545 550 555 560

Ser His Gly Gly Ser Asp Ala Phe Thr Val Ala Thr Cys Gln Gln Asp  
565 570 575

Val Ser Asp Phe His Val Asp Gly Asp Gly Val Asn Val Ile Arg Phe  
580 585 590

Gly Thr Lys Gln Thr Gly Asp Val Ser Leu Thr Leu Gly Leu Arg His  
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Gly Asp Phe  
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MBI15 Sequence Listing.ST25

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atc	tcc	gat	cca	tct	cct	acc	gac	gat	ttc	ttc	gag	cag	atc	ctc	ggg	218						
Ile	Ser	Asp	Pro	Ser	Pro	Thr	Asp	Asp	Phe	Phe	Glu	Gln	Ile	Leu	Gly							
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ctt	tcc	aac	ttc	tcc	ggt	tct	tca	ggt	tct	ggt	ctc	tct	gga	atc	ggc	266						
Leu	Ser	Asn	Phe	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Leu	Ser	Gly	Ile	Gly							
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ggc	gtg	ggt	cca	cct	ccg	atg	atg	ctt	cag	ctt	ggt	tca	ggc	aac	gaa	314						
Gly	Val	Gly	Pro	Pro	Pro	Met	Met	Leu	Gln	Leu	Gly	Ser	Gly	Asn	Glu							
	45					50					55											
ggg	aat	cat	aat	cat	atg	ggt	gcc	att	gga	gga	ggt	gga	cct	gta	ggg	362						
Gly	Asn	His	Asn	His	Met	Gly	Ala	Ile	Gly	Gly	Gly	Gly	Pro	Val	Gly							
60					65				70						75							
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Phe	His	Asn	Gln	Met	Phe	Pro	Leu	Gly	Leu	Ser	Leu	Asp	Gln	Gly	Lys							
			80						85				90									
gga	cat	ggc	ttt	ctt	aaa	cct	gat	gaa	act	ggt	aaa	cgt	ttc	caa	gac	458						
Gly	His	Gly	Phe	Leu	Lys	Pro	Asp	Glu	Thr	Gly	Lys	Arg	Phe	Gln	Asp							
			95					100					105									
gat	gtt	ctt	gat	aat	cga	tgt	tcc	tct	atg	aaa	cct	att	ttc	cat	ggg	506						
Asp	Val	Leu	Asp	Asn	Arg	Cys	Ser	Ser	Met	Lys	Pro	Ile	Phe	His	Gly							
		110					115					120										
cag	cca	atg	tca	cag	cca	gct	cca	cca	atg	ccg	cat	caa	cag	tct	act	554						
Gln	Pro	Met	Ser	Gln	Pro	Ala	Pro	Pro	Met	Pro	His	Gln	Gln	Ser	Thr							
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Ile	Arg	Pro	Arg	Val	Arg	Ala	Arg	Arg	Gly	Gln	Ala	Thr	Asp	Pro	His							
140					145					150					155							
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Ser	Ile	Ala	Glu	Arg	Leu	Arg	Arg	Glu	Arg	Ile	Ala	Glu	Arg	Ile	Arg							
				160				165						170								
tcg	ttg	cag	gaa	ctt	gta	cct	acc	gtt	aac	aag	aca	gat	agg	gct	gct	698						
Ser	Leu	Gln	Glu	Leu	Val	Pro	Thr	Val	Asn	Lys	Thr	Asp	Arg	Ala	Ala							
			175					180					185									
atg	atc	gac	gag	att	gtc	gat	tat	gta	aag	ttt	ctc	agg	ctc	caa	gtt	746						
Met	Ile	Asp	Glu	Ile	Val	Asp	Tyr	Val	Lys	Phe	Leu	Arg	Leu	Gln								

MBI15 Sequence Listing.ST25

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gcc gtg tgg gag aaa tgg tca aac gat ggg aca gag agg caa gtg gct				890
Ala Val Trp Glu Lys Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala	240	245	250	
aag ctg atg gaa gaa aac gtt gga gca gcg atg caa ctt ttg caa tca				938
Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser	255	260	265	
aag gct ctt tgc ata atg ccg atc tca ttg gca atg gcg att tac cat				986
Lys Ala Leu Cys Ile Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His	270	275	280	
tct cag cca cca gac aca tct tct tca atc gtc aaa cca gag atg aat				1034
Ser Gln Pro Pro Asp Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn	285	290	295	
cct cca ccg tag atttttgttc atccaacggc cccagctga tgattgacat				1086
Pro Pro Pro	300			
tttgctctgt ttcccactac tagacttttg tgactcatga aaggtaagta aaaaggcatt				1146
ggagatggaa tctaagtagg atttgtgcag taaagaagta aaacgggcatc tgtcaaaaga				1206
aggaaaaagc tctcgcttgc ttggctagta tttatcattt tgatgaaagt aactcttttt				1266
tgttcaaaga ctttagtggtg attttcagga ccaagggctt tgagggtagt gctagctgta				1326
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Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu Gly Asn His Asn His				
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Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly Phe His Asn Gln Met				
	65	70	75	80
Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly His Gly Phe Leu				
	85	90	95	
Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp Asp Val Leu Asp Asn				
	100	105	110	
Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly Gln Pro Met Ser Gln				
	115	120	125	
Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr Ile Arg Pro Arg Val				

MBI15 Sequence Listing.ST25

130	135	140	
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Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ser Leu Gln Glu Leu			
	165	170	175
Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp Glu Ile			
	180	185	190
Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu Ser Met			
	195	200	205
Ser Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr Glu Met			
	210	215	220
Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gln Ala Val Trp Glu Lys			
	225	230	240
Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu			
	245	250	255
Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Ile			
	260	265	270
Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp			
	275	280	285
Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn Pro Pro Pro			
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	Met Asp Tyr Lys Val Ser		
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aga agt ggg gag ata gta gaa gga gaa gta gaa gat tca gaa aag att			161
Arg Ser Gly Glu Ile Val Glu Gly Glu Val Glu Asp Ser Glu Lys Ile			
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gat tta cca cct ggt ttc aga ttt cac cca act gat gaa gaa ctt ata			209
Asp Leu Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile			
	25	30	35
aca cac tat cta aga cca aag gtt gta aac tct ttt ttc tct gct ata			257
Thr His Tyr Leu Arg Pro Lys Val Val Asn Ser Phe Phe Ser Ala Ile			
	40	45	50
gct att ggt gaa gtt gat ctc aac aaa gtc gag cct tgg gac ttg cct			305
Ala Ile Gly Glu Val Asp Leu Asn Lys Val Glu Pro Trp Asp Leu Pro			

MBI15 Sequence Listing.ST25

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Trp Lys Ala Lys Leu	Gly Glu Lys Glu Trp	Tyr Phe Phe Cys Val	Arg	
	75	80	85	
gac cga aaa tac ccg act	ggt tta aga acg aat	cgt gct act aaa gcc		401
Asp Arg Lys Tyr Pro Thr	Gly Leu Arg Thr Asn Arg	Ala Thr Lys Ala		
	90	95	100	
ggt tat tgg aaa gct aca	ggg aaa gat aaa gag	atc ttc aaa ggg aaa		449
Gly Tyr Trp Lys Ala Thr	Gly Lys Asp Lys Glu Ile	Phe Lys Gly Lys		
	105	110	115	
tct ctt gtt ggt atg aag	aaa aca ttg gtt ttc	tac aaa gga aga gct		497
Ser Leu Val Gly Met Lys	Lys Thr Leu Val Phe	Tyr Lys Gly Arg Ala		
	120	125	130	
cct aaa gga gta aaa aca	aat tgg gtc atg cat	gag tat cga tta gaa		545
Pro Lys Gly Val Lys Thr	Asn Trp Val Met His	Glu Tyr Arg Leu Glu		
	135	140	145	
ggc aaa ttc gct atc gat	aat ctc tct aaa acc	gct aag aac gaa tgt		593
Gly Lys Phe Ala Ile Asp	Asn Leu Ser Lys Thr	Ala Lys Asn Glu Cys		
	155	160	165	
gtt att agt cgt gtt ttt	cat aca cgg act gat	ggt acg aag gag cat		641
Val Ile Ser Arg Val Phe	His Thr Arg Thr Asp	Gly Thr Lys Glu His		
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Met Ser Val Gly Leu Pro	Pro Leu Met Asp Ser	Ser Pro Tyr Leu Lys		
	185	190	195	
agt aga gga caa gac tct	tta gcc ggg acc acc	ctt ggt ggg ttg ttg		737
Ser Arg Gly Gln Asp Ser	Leu Ala Gly Thr Thr	Leu Gly Gly Leu Leu		
	200	205	210	
tct cac gtt acc tac ttc	tcc gac caa aca acc	gat gac aag agt ctt		785
Ser His Val Thr Tyr Phe	Ser Asp Gln Thr Thr	Asp Asp Lys Ser Leu		
	215	220	225	
gtg gcc gat ttt aaa act	acc atg ttt ggt tcc	gga tcg act aac ttt		833
Val Ala Asp Phe Lys Thr	Thr Met Phe Gly Ser	Gly Ser Thr Asn Phe		
	235	240	245	
tta cca aac ata ggt tct	cta cta gac ttc gat	cct ctg ttt cta caa		881
Leu Pro Asn Ile Gly Ser	Leu Leu Asp Phe Asp	Pro Leu Phe Leu Gln		
	250	255	260	
aac aat tct tca gta ctg	aag atg ttg ctt gac	aat gaa gaa acc caa		929
Asn Asn Ser Ser Val Leu	Lys Met Leu Leu Asp	Asn Glu Glu Thr Gln		
	265	270	275	
ttt aag aag aat ctt cac	aat tca ggt tca tca	gag agt gaa cta aca		977
Phe Lys Lys Asn Leu His	Asn Ser Gly Ser Ser	Glu Ser Glu Leu Thr		
	280	285	290	
gcg agt tct tgg caa ggt	cac aat tct tat ggt	tcc act ggt cca gtg		1025
Ala Ser Ser Trp Gln Gly	His Asn Ser Tyr Gly	Ser Thr Gly Pro Val		
	295	300	305	
aat ctt gat tgc gtt tgg	aaa ttc tga atttgga	aaaaa tcgaaaattt		1072
Asn Leu Asp Cys Val Trp	Lys Phe			
	315			
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## MBI15 Sequence Listing.ST25

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Thr Asp Glu Glu Leu Ile Thr His Tyr Leu Arg Pro Lys Val Val Asn  
 35 40 45

Ser Phe Phe Ser Ala Ile Ala Ile Gly Glu Val Asp Leu Asn Lys Val  
 50 55 60

Glu Pro Trp Asp Leu Pro Trp Lys Ala Lys Leu Gly Glu Lys Glu Trp  
 65 70 75 80

Tyr Phe Phe Cys Val Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr  
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## MBI15 Sequence Listing.ST25

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MBI15 Sequence Listing.ST25

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Leu	Ile	Glu	His	Ser	Arg	Thr										
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## MBI15 Sequence Listing.ST25

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MBI15 Sequence Listing.ST25

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Gly Lys Asn Thr Gly Ala Met Thr Tyr Ser Phe Ile Lys Ala Val Lys	
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MBI15 Sequence Listing.ST25

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## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : A01H 1/00, 5/00; C12N 5/14, 15/82

US CL : 435/320.1, 419, 468; 800/278, 279, 287, 301, 305-310, 312, 314, 317, 320, 322

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 419, 468; 800/278, 279, 287, 301, 305-310, 312, 314, 317, 320, 322

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
EAST, USPAT; STN, Agricola, CaPlus, Biosis, Embase**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 97/47183 A1 (PURDUE RESEARCH FOUNDATION) 18 December 1997 (18.12.1997), entire reference.	1-9, 12, 13, 25 ----- 10, 11, 26, 27
X --- Y	US 5,939,601 (KLESSIG et al) 17 August 1999 (17.08.1999), entire reference.	1-9, 12, 13, 25 ----- 10, 11, 26, 27
A	Database Genbank on NCBI, US National Library of Medicine, (Bethesda, MD, USA) No. AB009055, SATO, S. et al 'Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned P1 and TAC clones. 27 December 2000, DNA RES. 1998, Vol. 5, No. 1, pages 41-54, see bases 16,003-16,490, 16,571-16,683 and 16,780-17,365.	1-13, 25-27



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

23 February 2001 (23.02.2001)

Date of mailing of the international search report

09 MAR 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

David Kruse

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PARALEGAL SPECIALIST  
TECHNOLOGY CENTER 1600

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claim Nos.: 14  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-13 & 25-27 and SEQ ID NOs 1&2

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31418

**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING** This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I-XXIX, claim(s) 1-14 and 25-27, drawn to a transgenic plant having modified seed characteristics, polynucleotides and vectors for producing said transgenic plant and a method of making said transgenic plant. Applicant must elect one pair of sequences (one nucleic acid and the corresponding amino acid translation) to be examined, *i.e.* SEQ ID NO: 1 and 2 in Group I, SEQ ID NO: 3 and 4 in Group II, SEQ ID NO: 5 and 6 in Group III, etc.

Group XXX, claim(s) 15-17, drawn to a method of identifying a factor that is modulated.

Group XXXI, claim(s) 18, drawn to a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide.

Group XXXII, claims(s) 19 and 20, drawn to an integrated computer system.

Group XXXIII, claim(s) 21-24, drawn to a method for identifying a polynucleotide sequence comprising selecting a nucleic acid sequence from a database that meets a selected sequence criteria.

The inventions listed as Groups I-XXXIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-XXXIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I-XXIX are drawn to a transgenic plant and a method of producing said plant with a nucleic acid sequence. The methods of Groups I-XXIX differ from each other in that they are directed to a plant transformation method and transgenic plant with a structurally and functionally distinct nucleic acid sequence which encodes a structurally and functionally distinct amino acid sequence. In addition, Groups XXX, XXXI and XXXIII are different methods from any of Groups I-XXIX in that they have different method steps and different end products, and Group XXXII requires a computer system. Thus, there is no single special technical feature, which links the inventions of Groups I-XXXIII under PCT Rule 13.2.